OM protein - protein search, using sw model

Run on: October 17, 2002, 16:35:40 ; Search time 20 Seconds
(without alignments)
1037.765 Million cell updates/sec

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GenCore version 5.1.3

Scoring table: BLOSUM62   Gapop 10.0 , Gapext 0.5

Sequence: 1 GLSHFCSGVIHVTKEVKEVA.........LRVNQTFNWNTTKQEHFPDN 216

Perfect score: 1149

Title: US-09-454-651B-23

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length %	DB	ID	Description
1	1149	100.0	288	2 A45803	B-cell-restricted
2	1085	94.4	289	2 G00031	B7 protein - red-c
3	738	64.2	299	2 I46690	CD80 precursor - r
4	601.5	52.3	321	2 I54696	B-lymphocyte activ
5	561	48.8	309	2 I49503	B-lymphocyte activ
6	185	16.1	275	2 JC7604	CD86 spliced varia
7	182	15.8	329	1 A48754	B7-2 antigen - hum
8	152	13.2	309	2 I49522	gene B7-2 protein
9	140.5	12.2	330	2 I46691	CD86 precursor - r
10	133.5	11.6	583	2 I39428	alcam - human
11	129	11.2	221	1 QOBE48	BARF1 protein - hu
12	127	11.1	526	2 S70587	butyrophilin precu
13	122.5	10.7	588	2 JH0506	adhesion molecule
14	122.5	10.7	588	2 A45254	surface glycoprote
15	120.5	10.5	509	2 JC5288	SHP substrate-1 pr
16	120.5	10.5	513	2 JC5289	SHP substrate-1 pr
17	118	10.3	487	2 S65133	butyrophilin - mou
18	116.5	10.1	1088	1 IJXLNL	neural cell adhesi
19	115	10.0	761	1 IJHUNG	neural cell adhesi
20	112.5	9.8	725	2 JE0099	neural cell adhesi
21	110.5	9.6	587	2 JH0464	DM-GRASP precursor
22	109.5	9.5	646	2 I38049	cell surface glyco
23	109.5	9.5	853	1 IJBONC	neural cell adhesi
24	109	9.5	526	1 A37821	butyrophilin - bov
25	109	9.5	2029	1 TDFFLK	protein-tyrosine-p
26	108	9.4	871	1 I48696	protein-tyrosine k
27	108	9.4	881	1 I48697	protein-tyrosine k
28	107.5	9.4	5175	2 T20992	hypothetical prote
29	107.5	9.4	5198	2 T43290	hemicentin precurs
30	106.5	9.3	333	2 A31923	amalgam protein pr
31	106.5	9.3	858	1 IJRTNC	neural cell adhesi
32	106	9.2	267	2 PL0064	T-cell receptor be
33	105.5	9.2	1091	1 IUCHNL	neural cell adhesi
34	104.5	9.1	210	2 A56169	Ig kappa chain V r
35	104	9.1	307	2 RWMSBC	T-cell receptor be
36	104	9.1	725	2 JE0100	neural cell adhesi
37	104	9.1	1092	1 JN0635	neural cell adhesi
38	103.5	9.0	408	2 A56182	fibroblast growth
39	103.5	9.0	725	1 IJMSNG	neural cell adhesi
40	103.5	9.0	1115	1 IJMSNL	neural cell adhesi
41	103	9.0	423	2 T29549	hypothetical prote
42	103	9.0	1273	2 JC5287	SHP substrate-1 pr
43	102.5	8.9	503	2 I50600	neogenin - chicken
44	102	8.9	1443	2 I50247	neogenin - chicken
45	101	8.8	1033	2 S19247	cell adhesion prot

ALIGNMENTS

RESULT 1

A45803

B-cell-restricted antigen B7 precursor - human
N;Alternate names: B-lymphocyte activation antigen B7
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Sep-1999
C;Accession: I54495; A45803
R;Selvakumar, A.; Mohanraj, B.K.; Eddy, R.L.; Shows, T.B.; White, P.C.; Dupont, B.
Immunogenetics 36, 175-181, 1992
A;Title: Genomic organization and chromosomal location of the human gene encoding the
A;Reference number: I54495; MUID:92307753
A;Accession: I54495
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-288 <RES>
A;Cross-references: GB:M83077; NID:g179327; PIDN:AAA58390.1; PID:g179329
R;Freeman, G.J.; Freedman, A.S.; Segil, J.M.; Lee, G.; Whitman, J.F.; Nadler, L.M.
J. Immunol. 143, 2714-2722, 1989
A;Title: B7, a new member of the Ig superfamily with unique expression on activated a
A;Reference number: A45803; MUID:90010147
A;Accession: A45803
A;Molecule type: mRNA
A;Residues: 1-288 <FRE>
A;Cross-references: GB:M27533; NID:g184680; PIDN:AAA36045.1; PID:g306916
A;Genetics:
A;Gene: GDB:CD80; CD28LG1; CD28
A;Cross-references: GDB:251792; OMIM:112203
A;Map position: 3q13.3-3q21
A;Introns: 34/1; 140/1; 234/1; 266/1
A;Superfamily: B-lymphocyte restricted antigen B7
C;Keywords: transmembrane protein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;248-264/Domain: transmembrane #status predicted <TMM>

Query Match   100.0%; Score 1149; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 2.1e-85;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy     61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy    121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy    181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
            ||||||||||||||||||||||||||||||||||||
```

```
Db    207 NMTTNHHSFMCLIKYGHLRVNQTFNWWNTIKQEHFPDN 242
```

RESULT 2
G00031
B7 protein - red-crowned mangabey (fragment)
C;Species: Cercocebus torquatus (red-crowned mangabey, white-collared mangabey)
A;Reference number: G00031
C;Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 29-Sep-1999
C;Accession: G00031
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-289 <VIL>
A;Cross-references: EMBL:U19833; NID:g644783; PIDN:AAA86700.1; PID:g644784
A;Gene: B7
C;Genetics:
C;Superfamily: B-lymphocyte restricted antigen B7

Query Match   94.4%;   Score 1085;   DB 2;   Length 289;
Best Local Similarity   95.3%;   Pred. No. 3.1e-80;
Matches 205;   Conservative 4;   Mismatches 6;   Indels 0;   Gaps 0;

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Qy    2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 61
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 87

Qy   62 KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   88 KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 147

Qy  122 SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  148 TDFEIPPSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 207

Qy  182 MTTNHSFMCLIKYGHLRVNQTFNWWNTIKQEHFPDN 216
         ||||||||||||||||||||||||||||||||||||
Db  208 MTTNHSFVCLIKYGHLRVNQTFNWWNTPKQEHFPDN 242
```

RESULT 3
I46690
CD80 precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999
C;Accession: I46690
R;Isono, T.; Seto, A.
A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecul
A;Reference number: I46690; MUID:95369849
A;Accession: I46690
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-299 <ISO>
A;Cross-references: GB:D49843; NID:g755096; PIDN:BAA08643.1; PID:g755097
C;Superfamily: B-lymphocyte restricted antigen B7

Query Match   64.2%;   Score 738;   DB 2;   Length 299;
Best Local Similarity   63.9%;   Pred. No. 3.3e-52;
Matches 133;   Conservative 36;   Mismatches 39;   Indels 0;   Gaps 0;

```
Qy    4 HFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKN 63
         ||||||||||||||||||::||||||||||::|::|:||||||||||||||||||||||
Db   29 HFSSGISQVTKSVKEMAALSCDYNISIDELARMRIYWQKDQQMVLSIISGQVEVWPEYKN 88

Qy   64 RTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISD 123
         |||||||||||||||:||||||||||||:||:|||||||||||||:||||||||:::::
Db   89 RTFPDITNNLSLMILALRLSDKGTYTCVVQKNENGSFRREHLTSVTLSIRADFPVPSITD 148

Qy  124 FEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMT 183
         ||::||:|||||||||||||||||||:|| || ||||:||||:|||::|||||||:|||:
```

```
Db  149 IGHPDNVKRIRCSASGGFPEPRLAWMEDGEELNAVNTTVDQDLDTELYSVSSELDFNVT 208

Qy  184 TNHSFMCLIKYGHLRVNQTFNWWNTTKQE 211
         :||:|| ||:|:|:|:||:|:
Db  209 NNHSIVCLIKYGELSVSQIFPWSKPKQE 236
```

RESULT 4
I54766
B-lymphocyte activation antigen 7-1 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 19-May-2000
C;Accession: I54766
R;Judge, T. A.; Liu, M.; Christensen, P. J.; Fak, J. J.; Turka, L. A.
Int. Immunol. 7, 171-178, 1995
A;Title: Cloning the rat homolog of the CD28/CTLA-4-ligand B7-1: structural and funct
A;Reference number: I54766; MUID:95252184
A;Accession: I54766
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-321 <RES>
A;Cross-references: EMBL:U05593; NID:g453381; PIDN:AAA80154.1; PID:g453382
C;Superfamily: B-lymphocyte restricted antigen B7

Query Match   52.3%;   Score 601.5;   DB 2;   Length 321;
Best Local Similarity   54.4%;   Pred. No. 3.7e-41;
Matches 112;   Conservative 35;   Mismatches 58;   Indels 1;   Gaps 1;

```
Qy    1 GLSHFCSGVI-HVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWP 59
         |||| ||| | |||:||  ||||||||::|||||||:||||:|||||||||||||||||
Db   31 GLLQISSGIVGQVSKSVREKALLSCDYKFCSEEQSIHRIYWQKHDKMVLSVISGVPEVWP 90

Qy   60 EYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTP 119
         |||:|:|::|:||||||||||||||:||||||||||||||||||||||:||||||::|
Db   91 KYKNRTVYDIANNYSFSLLGLILSDRGTYTYCVVQRYEGGSYVVKIHLTTVELSVRADFPTP 150

Qy  120 SISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 179
         :|:: ||||:||||||||||||||||||||||||||||||:|||||||::|||||||||
Db  151 NITEYGNPSADIKRITCFASGGFPKPRLSWLENGRELNGINTTISQPESELYTISSQLD 210

Qy  180 FNMTTNHSFMCLIKYGHLRVNQTFNWW 205
         ||| ::|:|| ||:|:|:|:||:|:
Db  211 FNATYDHFIDCFIEYGDAHVSQNFTW 236
```

RESULT 5
I49503
B-lymphocyte activation antigen 7 precursor - mouse
N;Alternate names: MB7-2
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C;Accession: I49503; S17291; I49521
R;Selvakumar, A.; White, P. C.; Dupont, B.
Immunogenetics 38, 292-295, 1993
A;Title: Genomic organization of the murine B-lymphocyte activation antigen B7.
A;Reference number: I49503; MUID:9307789
A;Accession: I49503
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-309 <RES>
A;Cross-references: GB:L12589; NID:g293299; PIDN:AAA37240.1; PID:g293301
R;Freeman, G. J.; Gray, G. S.; Gimmi, C. D.; Lombard, D. B.; Zhou, L. J.; White, M.; Finge
J. Exp. Med. 174, 625-631, 1991
A;Title: Structure, expression, and T cell costimulatory activity of the murine homol
A;Reference number: I49503; S17291; MUID:91341422
A;Accession: S17291
A;Residues: 1-274, R',279-309 <FRE>
A;Cross-references: EMBL:X60958; NID:g50111; PIDN:CAA43291.1; PID:g50112
R;Inobe, M.; Linsley, P. S.; Ledbetter, J. A.; Nagai, Y.; Tamakoshi, M.; Uede, T.
Biochem. Biophys. Res. Commun. 200, 443-449, 1994
A;Title: Identification of an alternatively spliced form of the murine homologue of B
A;Reference number: I49521; MUID:94220123

A:Accession: I49521
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-143,238-274,'R',279-309 <RE2>
A:Cross-references: GB:D16220; NID:g505118; PIDN:BAA03748.1; PID:g994769
A:Genetics:
A:Gene: B7
A:Introns: 37/1; 143/1; 237/1; 275/1
A;Superfamily: B-lymphocyte restricted antigen B7
C;Keywords: alternative splicing

```
Query Match              48.8%;  Score 561; DB 2;  Length 309;
Best Local Similarity    50.7%;  Pred. No. 6.6e-38;
Matches  104;  Conservative  41;  Mismatches  58;  Indels   2;  Gaps   2;

Qy   12 VTKEVEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRTIFDITN 71
           :|:|||  | ||:|  |||||  ||||||||||||| ||:||||||||||||||||:
Db   42 LSKSVKDKVLLPCRYNSPHEDESEDRIYWQKHDKVVLSVIAGKLKVWPEYKNRTLYDNT- 100

Qy   72 NLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNI 131
         ||:|||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db  101 TYSLIILGLVLSDRGTYSCVVQKKERGTYEVKHLALVLKISIKADFSTPNITEGGNPSADT 160

Qy  132 RRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSFMCL 191
          |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db  161 KRITCFASGGFPKPRFSWLENGRELPGINTTISQDPESELYTISSQLDFNTTRNHTIKCL 220

Qy  192 IKYGHLRVNQTFNWNNTKQEHFPDN 216
          ||| |  ||::| |||  ||  ||
Db  221 IKYGDAHVSEDFTWEKPFEDP-PDS 244
```

RESULT 6
JC7604
CD86 spliced variant CD86 deltaTM isoform - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001
C;Accession: JC7604
R;Magistrelli, G.; Caron, G.; Gauchat, J.F.; Jeannin, P.; Bonnefoy, J.Y.; Delneste, Y.
Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001
A;Title: Identification of an alternatively spliced variant of human CD86 mRNA.
A;Reference number: JC7604; MUID:21092744; PMID:11162656
A;Accession: JC7604
A;Molecule type: mRNA
A;Residues: 1-275 <MAG>
C;Comment: This CD86 variant expressed by activated human monocytes, is a costimulatory
C;Genetics:
A;Gene: cd86deltaTM
C;Keywords: immune response

```
Query Match              16.1%;  Score 185; DB 2;  Length 275;
Best Local Similarity    27.4%;  Pred. No. 1.3e-07;
Matches   65;  Conservative  42;  Mismatches  78;  Indels  52;  Gaps  12;

Qy   18 EVATLSC---GHNVSVEELAQTRIYWQKEKKMVLTMM--SGDMNIWPEYKNRTIFDI 69
         ||   |     |||  || ||:|| | |||| :|      |||||:|||||||||
Db   28 ETADLPCQFANSQNQSLSELV--VFWQDQENLVLNEVYLGRKFDSVHSKYMGRTSFD- 83

Qy   70 TNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTS 129
         |:: ||:| ||||:||||:||:||  | |||||||||||:|||||||||||||||||
Db   84 SDSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRIHQMNSELSVLANFSQPEI---VPIS 139

Qy  130 NIR-----RIICSTSGGFPEP-HLSWLENGEELNAINTTV------SQDPETELYAVS 175
         ||      |||||||||||||  |||||||||||||||||       ||||||||||
Db  140 NITENVYINLICSSIHGYPEPKKMSVL----LRTKNSTIEYDGIMQKSQDNVTELYDVS 194

Qy  176 SKLDF---NMTTNHSFMCLIKYGHLRVNQ---TFNWNNTTKQE------HFPD 215
         :|||     |:|||||| ||:|||:||||    ||||||||||       ||
Db  195 ISLSVSFPDVTSNMTIFCILETDKTRLLSSPFSIGTNTMERESEQTKKREKIHPE 251
```

RESULT 7
A48754

B7-2 antigen - human
N;Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A48754; S39055
R;Freeman, G.J.; Gribben, J.G.; Boussiotis, V.A.; Ng, J.W.; Restivo Jr., V.A.; Lombar
Science 262, 909-911, 1993
A;Title: Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell pr
A;Reference number: A48754; MUID:94053735
A;Accession: A48754
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-329 <FRE>
A;Cross-references: GB:L25259; NID:g416368; PIDN:AAA58389.1; PID:g416369
R;Azuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L.L.; Somoza,
Nature 366, 76-79, 1993
A;Note: it is uncertain whether Met-1 or Met-7 is the initiator
A;Title: B70 antigen is a second ligand for CTLA-4 and CD28.
A;Reference number: S39055; MUID:94050123
A;Accession: S39055
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 7-329 <AZU>
A;Cross-references: GB:U04343; NID:g439838; PIDN:AAB03814.1; PID:g439839
A;Genetics:
A;Gene: GDB:CD86; CD28LG2
A;Cross-references: GDB:433597; OMIM:601020
A;Map position: 3q13.3-3q21
A;Superfamily: B7-2 antigen
C;Keywords: glycoprotein

```
Query Match              15.8%;  Score 182; DB 1;  Length 329;
Best Local Similarity    29.0%;  Pred. No. 2.7e-07;
Matches   60;  Conservative  38;  Mismatches  71;  Indels  38;  Gaps  10;

Qy   18 EVATLSC---GHNVSVEELAQTRIYWQKEKKMVLTMM---SGDMNIWPEYKNRTIFDI 69
         ||   |     |||  || ||:|| | |||| :|       |||||:|||||||||
Db   34 ETADLPCQFANSQNQSLSELV---VFWQDQENLVLNEVYLGKEKFDSVHSKYMGRTSFD- 89

Qy   70 TNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTS 129
         |:: ||:| ||||:||||:||:||  | |||||||||||:|||||||||||||||||
Db   90 SDSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRIHQMNSELSVLANFSQPEI---VPIS 145

Qy  130 NIR-----RIICSTSGGFPEP-HLSWLENGEELNAINTTV------SQDPETELYAVS 175
         ||      |||||||||||||  |||||||||||||||||       ||||||||||
Db  146 NITENVYINLICSSIHGYPEPKKMSVL----LRTKNSTIEYDGIMQKSQDNVTELYDVS 200

Qy  176 SKLDF---NMTTNHSFMCLIKYGHLRV 199
         :|||     |:|||||| ||:|||:||
Db  201 ISLSVSFPDVTSNMTIFCILETDKTRL 227
```

RESULT 8
I49522
gene B7-2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: I49522
R;Freeman, G.J.; Borriello, F.; Hodes, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Kim
J. Exp. Med. 178, 2185-2192, 1993
A;Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell
A;Reference number: I49522; MUID:94065585
A;Accession: I49522
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-309 <RES>
A;Cross-references: GB:L25606; NID:g432478; PIDN:AAA79770.1; PID:g432479
C;Genetics:
A;Gene: B7-2
C;Superfamily: B7-2 antigen

```
Query Match              13.2%;  Score 152; DB 2;  Length 309;
Best Local Similarity    26.1%;  Pred. No. 6.7e-05;
```

```
Matches   52;  Conservative   43;  Mismatches   78;  Indels   26;  Gaps   10;

Qy    20  ATLSCG---GHNVSVEELAQTRIYWQKEKKMVL------TMMSGDMNIWPEYKNRTIFDI   69
              | ||      :||  | |:| :||||  ||  |         | | | :   |   |
Db    36  AVLPCFTKAQNISLSELV--VFWQDQKILVLEYHYLGTEKLDSVN--AKYLGRTSPD-    89

Qy    70  TNNLSIVILALRPSDEGTYECVVLKYEK--DAFKREHLAEVTLSVKADFPPTSISDFEIP  127
          :||   | |:  | ::  :| | :|   |  :  |     |  :  |   |   ||
Db    90  RNNWTLRLHNVQIKDMGSVDCFIQKKPPTGSIILQQTLTE--LSVLANFSDPEIKLAQNV  147

Qy   128  TSNIK-RICSTSGGFPEPHLSW--LENGEELNAINTTVSQDPETELYAVSSKLDFNM--  182
          |:|    |  ||  :      :  |    :|       :|  |   |:    :
Db   148  TGNSGINLTCTSKQGHPKPKKMYFLITNSTNEYGDNMQISODNVIELFSINSLSLSFPD  207

Qy   183  -TTNHSFMCLIKYGHLRVN   200
           |||| | |||:||  :
Db   208  GVWHMTVVCVLETESMKIS   226
```

RESULT 9
I46691
CD86 precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 23-Jul-1999
C;Accession: I46691
R;Isono, T.; Seto, A.
A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecul...
A;Immunogenetics 42, 217-220, 1995
A;Reference number: I46689; MUID:9536849
A;Accession: I46691
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-330 <ISO>
A;Cross-references: GB:D49842; NID:g755098; PIDN:BAA08642.1; PID:g755099
C;Superfamily: B7-2 antigen

Query Match   12.2%; Score 140.5; DB 2; Length 330;
Best Local Similarity   27.4%; Pred. No. 0.00062;
Matches   60; Conservative   34; Mismatches   84; Indels   41; Gaps   12;

```
Qy    18  EVATLSCGH-NVSVEELAQTRIYWQKEKKMVLIMM----SGDMNIWPEYKNRTIFDITN-   71
              ||| | :|  | :::  | |||||  ||  |        |   |  | : :|  |
Db    34  KTADLPCQFTNSQSRSLSELVFWQDQKILVLELFLGREKPDNVDPKYIGRTSPDQESW    93

Qy    72  NLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTSISDFEIPTSNI  131
Db    94  NLQLHNVQIK--DKGVYQCFVHHRGAKGLVPIYQMNSELSVLANFTQPEITT------LISNI  147

Qy   132  RR-------IICSTSGGFPEPHLSWLENGEELNAINTTV------SQDPETELY--AVSS  176
Db   148  TRNSAINLTCSSVQGYPEPKKMFF------VLKTENATTEYDGVIEKSQDNVTGLYNISISG  203

Qy   177  KLDF-NMTTNHSFMCLIKYGHLRVNQFPNWNTIKQEHP  214
Db   204  SITFSDDIRNAIIYCVL--------QTESTETYSQ-HFP  233
```

RESULT 10
I39428
alcam - human
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C;Accession: I39428
R;Bowen, M.A.; Patel, D.D.; Li, X.; Modrell, B.; Malacko, A.R.; Wang, W.C.; Marquardt, H...
J. Exp. Med. 181, 2213-2220, 1995
A;Title: Cloning, mapping, and characterization of activated leukocyte-cell adhesion mol...
A;Accession: I39428
A;Reference number: I39428; MUID:95279947
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-583 <RES>
A;Cross-references: GB:L38608; NID:g886257; PIDN:AAB59499.1; PID:g886258

Query Match   11.6%; Score 133.5; DB 2; Length 583;
Best Local Similarity   24.5%; Pred. No. 0.0046;
Matches   37; Conservative   35; Mismatches   54; Indels   25; Gaps   7;

```
Qy    59  PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPT  118
Db    84  PEYKDR--LNLSENYTLSISNARISDEKRFVCMLVT-EDNVFEAPTIVKV------FKQ   133

Qy   119  PSISDFE-----IPTSNIRRI-ICSTSGGFPEPHLSWLENGEELNAINTTV------SQD  166
Db   134  PSKPEIVSKALFLETEQLKKLGDCISEDSYPDGNITWYRNGKVLHPLEGAVVIIFKKEMD  193

Qy   167  PETELYAVSSKLDFNMT----TNHSFMCLIKY  194
Db   194  PVTQLIYTMTSTLEYKYTTKADIIQMPFTCSVTY  224
```

RESULT 11
QOB48
BARF1 protein - human herpesvirus 4 (strain B95-8)
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999
C;Accession: B43045; A03792; S33058
R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
A;Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr vi...
A;Mol. Biol. Med. 1, 21-45, 1983
A;Reference number: A93065; MUID:85035713
A;Accession: B43045
A;Molecule type: DNA
A;Residues: 1-221 <BAN>
A;Cross-references: EMBL:V01555; NID:g59074; PIDN:CAA24809.1; PID:g1334917
R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J...
A;Nature 310, 207-211, 1984
A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A;Reference number: A03794; MUID:84270667
A;Contents: annotation; protein coding region
C;Superfamily: human herpesvirus 4 BARF1 protein

Query Match   11.8%; Score 129; DB 1; Length 221;
Best Local Similarity   27.0%; Pred. No. 0.0031;
Matches   43; Conservative   25; Mismatches   47; Indels   44; Gaps   8;

```
Qy    18  EVATLSCGHNVSVEELAQTRIYWQK-------------EKKMVLTMMSGDMNIWPE     60
Db    19  QAVTAFLGERVTLTS-----YWRRVSLGPEIEVSWFKLGPGEEQVLIGRMHHDV-IFIE  71

Qy    61  YKNRTIFDI---TNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEV---TLSV--  112
Db    72  WPFRGFFDIHRSANTFLVVTAANISHDGNYLCRMKLGETEVTKQEHLSVVKPLTLSVHS  131

Qy   113  -KADFPPTSISDFEIPTSNIRRICSTSGGFPEPHLSWL  150
Db   132  ERSOFP-----DFSVLT-----VTCTVNAFPHFHVQWL  159
```

RESULT 12
S70587
butyrophilin precursor - human
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C;Accession: S70587
R;Taylor, M.R.; Peterson, J.A.; Ceriani, R.L.; Couto, J.R.
A;Title: Cloning and sequence analysis of human butyrophilin reveals a potential rece...
Biochim. Biophys. Acta 1306, 1-4, 1996
A;Reference number: S70587; MUID:96201696
A;Accession: S70587
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-526 <TAY>
A;Cross-references: EMBL:U39576; NID:g1326082; PIDN:AAC50489.1; PID:g1326083

Query Match   11.8%; Score 127; DB 2; Length 526;
Best Local Similarity   27.5%; Pred. No. 0.014;

Matches   52;   Conservative   33;   Mismatches   84;   Indels   20;   Gaps   10;

```
Qy   16 VKEVATLSC--GHNVSVEELAQTRIVWQKEKKMVLTMMSG---DMNIWPEYKNRTIF---  67
           :|| |:||     ::  |   |  |||    | : || :        :  ||| ::|
Db   42 VGEDAELPCRLSPNASAEHL-ELRWFRKKVSPAVLVHRDGREQEAEQMPEYRGRATLVQD 100

Qy   68 -DITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDPEI 126
          ||  :  |  |   : | | | |:      |::     |  :|:          ::
Db  101 GIAKGRVALRIRGVRVSDDGEYTCF---FREDGSYEEAL--VHLKVAALGSDPHIS-MQV 154

Qy  127 PTSNIRRIICSTSGGFPEPHLSW-LENGEELNAINITVSQDPETE-LYAVSSKLDFNMTT 184
          :   |  | |:|  | |  : |   || :        :      :  | :
Db  155 QENGEICLECTSVGWYPEPQVQWRTSKGEKFP--STSESRNPEEGLFTVAASVIIRDTS 212

Qy  185 NHSFMCLIK 193
          : |||| :
Db  213 TKNVSCYIQ 221
```

RESULT 13
JH0506
adhesion molecule SC1 precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date:31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jul-2000
R;Tanaka, H.; Matsui, T.; Agata, A.; Tomura, M.; Kubota, I.; McFarland, K.C.; Kohr, B.;
Neuron 7, 535-545, 1991
A;Title: Molecular cloning and expression of a novel adhesion molecule, SC1.
A;Reference number: JH0506; MUID:92030150
A;Molecule type: mRNA
A;Residues: 1-588 <TAN>
A;Cross-references: GB:S63276; NID:g238000; PIDN:AAB20170.1; PID:g238001
A;Experimental source: embryo
A;Contents: embryo
A;Accession: PS0270
A;Molecule type: protein
A;Residues: 34-48 <TAN>
C;Comment: This protein is uniquely and transiently expressed on spinal cord motoneurons
C;Keywords: glycoprotein; transmembrane protein
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-588/Product: adhesion molecule SC1 #status predicted <MAT>
F;500-523/Domain: transmembrane #status predicted <TRA>
F;101,173,199,271,312,366,462,485,504/Binding site: carbohydrate (Asn) (covalent) #statu

Query Match   10.7%;   Score 122.5;   DB 2;   Length 588;
Best Local Similarity   25.7%;   Pred. No. 0.036;
Matches   39;   Conservative   32;   Mismatches   54;   Indels   27;   Gaps   8;

```
Qy   59 PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPT 118
          | |::   |  :   ||::  | ||:  | :|::    :   |:    : :| ||
Db   90 PDYKDR--LSLSENYTLSIKNARISDEKRFVCMLVT-EDDVSEEPTVKV-----FKQ 139

Qy  119 PS------ISDFEIPTSNIRRI-ICSTSGGFPEPHLSWLENG-----EELNAINITVSQ 165
          |       :||:   : |    |  :  | ||  : | ||          | |:  :|
Db  140 PSQPEILHQADF-LETEKLKMLGECVVRDSYPEGNVTWYKNGRVLQPVEEVVVINLRKVE 198

Qy  166 DPETELYAVSSKLDFNMT---TNHSFMCLIKY 194
          :  :  |  :| | :| |   ||  |  |: |
Db  199 NRSTGLFTMTSSLQYMPTKEDANAKFTCIVTY 230
```

RESULT 14
A45254
surface glycoprotein BEN precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jul-2000
C;Accession: A45254; S19202
R;Pourquie, O.; Corbel, C.; Le Caer, J.P.; Rossier, J.; Le Douarin, N.M.
Proc. Natl. Acad. Sci. U.S.A. 89, 5261-5265, 1992
A;Title: BEN, a surface glycoprotein of the immunoglobulin superfamily, is expressed in
A;Reference number: A45254; MUID:9302224
A;Accession: A45254
A;Status: preliminary

A;Molecule type: mRNA
A;Residues: 1-588 <POU>
A;Cross-references: EMBL:X64301; NID:g63087; PIDN:CAA45579.1; PID:g63088
C;Keywords: glycoprotein

Query Match   10.7%;   Score 122.5;   DB 2;   Length 588;
Best Local Similarity   25.7%;   Pred. No. 0.036;
Matches   39;   Conservative   32;   Mismatches   54;   Indels   27;   Gaps   8;

```
Qy   59 PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPT 118
          | |::   |  :   ||::  | ||:  | :|::    :   |:    : :| ||
Db   90 PDYKDR--LSLSENYTLSIKNARISDEKRFVCMLVT-EDDVSEEPTVKV-----FKQ 139

Qy  119 PS------ISDFEIPTSNIRRI-ICSTSGGFPEPHLSWLENG-----EELNAINITVSQ 165
          |       :||:   : |    |  :  | ||  : | ||          | |:  :|
Db  140 PSQPEILHQADF-LETEKLKMLGECVVRDSYPEGNVTWYKNGRVLQPVEEVVVINLRKVE 198

Qy  166 DPETELYAVSSKLDFNMT---TNHSFMCLIKY 194
          :  :  |  :| | :| |   ||  |  |: |
Db  199 NRSTGLFTMTSSLQYMPTKEDANAKFTCIVTY 230
```

RESULT 15
JC5288
SHP substrate-1 protein, 509 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
C;Accession: JC5288
R;Yanao, T.; Matozaki, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioka,
Biochem. Biophys. Res. Commun. 231, 61-67, 1997
A;Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localizat
A;Reference number: JC5287; MUID:97223399
A;Contents: Brain
A;Accession: JC5288
A;Molecule type: mRNA
A;Residues: 1-509 <YAM>
A;Cross-references: DDBJ:D87967; NID:g1864012; PIDN:BAA13520.1; PID:g1864013
C;Comment: This protein is a glycosylated receptor-like protein and plays a role in c
acts as a docking protein and induce translocation of SHP-2 from the cytosol to the
C;Genetics:
A;Gene: shps-1
A;Map position: 2

Query Match   10.8%;   Score 120.5;   DB 2;   Length 509;
Best Local Similarity   25.9%;   Pred. No. 0.044;
Matches   59;   Conservative   42;   Mismatches   88;   Indels   39;   Gaps   15;

```
Qy    3 SHFCSGV-----IHVTKEVKEVA-------TLSCGHNVSVEELAQTRIVWQK--EKKMVL  48
          | ||:||     ||::|| | |         ::|| |  |   |  |||    |||| |
Db   23 SCFCTGVTGKELKVTQPERKSVSVAAGDSTVLNC---TLTSLLPVGPIKWVRGVGQSRLLI 79

Qy   49 TMMSGDMNIWPEYKNRTIFDIT--NNL--SIVILALRPSDEGTYECVVLKYEKDAFKREH 104
           :  || ||  | |::   |  :       :  ::|| | | | :   | : : :   |
Db   80 YSFTGEH--FPRVIN--VSDATKRNNMDFSIRISNVTPEDAGTTYCV--KFQKGPSEPDT 133

Qy  105 L------AEVTLSVKADFPTPS-ISDFEIPTSNIRRIICSTSGGFPEP-HLSWLENGEEL 156
                  :|: | |  :   || :||:   : |  |  |  :  | ||  : | ||
Db  134 EIQSGGGTEVYVLAKPSPPEVSGPADRGIPDQKV-NFTCKSHGFSPRNTILKWFRDGQEL 192

Qy  157 NAINTTVSQDPETELYAVSS--KLDFNMTTNHSFMCLIKYGHLRVNQT 202
           | :|||: |  : |  :|    || ::| :|  |  |: | | |: |
Db  193 HHLETTVNPSGKNVSYNISSTVRVVLNSMDVHS-KVICEVAHITLDRS 239
```

Search completed: October 17, 2002, 16:37:21
Job time : 22 secs

OM protein - protein search, using sw model

GenCore version 5.1.3
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Run on: October 17, 2002, 16:35:40 ; Search time 13 seconds
                 (without alignments)
                 643.340 Million cell updates/sec

Title: US-09-454-651B-23
Perfect score: 1149
Sequence: 1 GLSHFCSGVIHVTKEVKEVA.........LRVNQTFNWNTTKQEHFPDN 216

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Accession	Description
1	1149	100.0	288	1	CD80_HUMAN	P33681	homo sapien
2	738	64.2	299	1	CD80_RABIT	P42070	oryctolagus
3	561	48.8	306	1	CD80_MOUSE	Q00609	mus musculu
4	182	15.8	329	1	CD86_HUMAN	P42081	homo sapien
5	161	14.0	302	1	ICOL_HUMAN	O75144	homo sapien
6	152	13.2	309	1	CD86_MOUSE	P42082	mus musculu
7	150.5	13.1	322	1	ICOL_MOUSE	Q9jh38	mus musculu
8	134.5	12.2	330	1	CD86_RABIT	P42071	oryctolagus
9	134.5	11.7	583	1	NCA2_MOUSE	Q61490	mus musculu
10	133.5	11.6	583	1	C166_HUMAN	Q13740	homo sapien
11	129	11.2	221	1	BRF1_EBV	P03228	epstein-bar
12	127	11.1	526	1	BUTY_HUMAN	Q13410	homo sapien
13	122.5	10.7	588	1	C166_CHICK	P42292	gallus gall
14	119	10.4	524	1	BUTY_MOUSE	O62556	mus musculu
15	116.5	10.1	1088	1	NCA1_XENLA	P16170	xenopus lae
16	115	10.1	761	1	NCA2_HUMAN	P13592	homo sapien
17	115	10.0	848	1	NCA1_HUMAN	P13591	homo sapien
18	110.5	10.0	321	1	NCA1_HUMAN	P13591	homo sapien
19	109.5	9.6	646	1	TCB_FLV	P43121	feline leuk
20	109.5	9.5	853	1	MU18_HUMAN	P31364	homo sapien
21	109	9.5	526	1	NCA1_BOVIN	P31836	bos taurus
22	109	9.5	2029	1	NCA2_BOVIN	P18892	bos taurus
23	108.5	9.4	365	1	LAR_DROME	P16621	drosophila
24	107.5	9.4	333	1	AMAL_DROME	P97792	drosophila
25	106.5	9.3	858	1	NCA1_RAT	P15364	rattus norv
26	106.5	9.3	319	1	NCA1_CHICK	P13596	gallus gall
27	105	9.1	1091	1	A33_HUMAN	P13596	homo sapien
28	105	9.1	1091	1	NCA1_CHICK	Q99795	gallus gall
29	104	9.1	725	1	NCA2_CHICK	Q13590	gallus gall
30	103.5	9.0	1115	1	NCA2_XENLA	Q13590	xenopus lae
31	103.5	9.0	1115	1	CXAR_MOUSE	P36335	mus musculu
32	103	9.0	298	1	JAM2_HUMAN	P57087	homo sapien
33	102	8.9	1443	1	NEO1_CHICK	Q90610	gallus gall
34	101.5	8.8	403	1	RAGE_MOUSE	O62151	mus musculu
34	100	8.7	413	1	HEMO_MANSE	P31398	manduca sex
35	99.5	8.7	1338	1	VGR1_HUMAN	P17948	homo sapien
36	98.5	8.6	365	1	CXAR_HUMAN	P78310	homo sapien
37	98	8.5	278	1	OX2G_RAT	P04218	rattus norv
38	98	8.5	298	1	JAM1_BOVIN	Q9xt56	bos taurus
39	98	8.4	1333	1	VGR1_MOUSE	P35969	mus musculu
40	97	8.4	1336	1	VGR1_RAT	P53767	rattus norv
41	96.5	8.4	739	1	VCA1_HUMAN	P19320	homo sapien
42	96	8.4	1020	1	CONT_MOUSE	P12960	mus musculu
43	95.5	8.3	811	1	FS22_DROME	P34083	drosophila
44	95.5	8.3	873	1	FS21_DROME	P34082	drosophila
45	95.5	8.3	1348	1	VGR2_COTJA	P52583	coturnix co

ALIGNMENTS

RESULT 1
CD80_HUMAN

```
ID   CD80_HUMAN     STANDARD;      PRT;   288 AA.
AC   P33681;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T lymphocyte activation antigen CD80 precursor (Activation B7-1
DE   antigen) (CTLA-4 counter-receptor B7.1) (B7) (BB1).
GN   CD80 OR CD28LG1 OR CD28LG OR LAB7.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphoid;
RX   MEDLINE=90010147; PubMed=2794510;
RA   Freeman G.J., Freedman A.S., Segil J.M., Lee G., Whitman J.F.,
RA   Nadler L.M.;
RT   "B7, a new member of the Ig superfamily with unique expression on
RT   activated and neoplastic B cells.";
RL   J. Immunol. 143:2714-2722(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92307753; PubMed=1377173;
RA   Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C.,
RA   Dupont B.;
RT   "Genomic organization and chromosomal location of the human gene
RT   encoding the B-lymphocyte activation antigen B7.";
RL   Immunogenetics 36:175-181(1992).
RN   [3]
RP   SEQUENCE OF 35-38.
RX   MEDLINE=91341422; PubMed=1714935;
RA   Freeman G.J., Gray G.S., Gimmi C.D., Lombard D.B., Zhou L.-J.,
RA   White M., Fingeroth J.D., Gribben J.G., Nadler L.M.;
RT   "Structure, expression, and T cell costimulatory activity of the
RT   murine homologue of the human B lymphocyte activation antigen B7.";
RL   J. Exp. Med. 174:625-631(1991).
RN   [4]
RP   CHARACTERIZATION.
RX   MEDLINE=95088403; PubMed=7527824;
RA   Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,
RA   Okumura K., Ito D., Azuma M.;
RT   "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T
RT   cell proliferation, and T cell costimulatory activity of the
RT   cell proliferation, cytokine production, and generation of CTL.";
RL   J. Immunol. 154:97-105(1995).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 35-234.
RX   MEDLINE=20125021; PubMed=10651405;
RA   Ikemizu S., Gilbert R.J., Fennelly J.A., Collins A.V., Harlos K.,
RA   Jones E.Y., Stuart D.I., Davis S.J.;
RT   "Structure and dimerization of a soluble form of B7-1.";
RL   Immunity 12:51-60(2000).
CC   -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
CC       LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
```

```
CC        PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
CC        RECEPTOR.
CC   -!-  SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!-  TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, MACROPHAGES
CC        AND DENDRITIC CELLS.
CC   -!-  SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!-  SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!-  SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC   -!-  DATABASE: NAME=PROW; NOTE=CD guide CD80 entry;
CC        WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd80.htm".
CC
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
DR   EMBL; M27533; AAA36045.1; -.
DR   EMBL; M83077; AAA58390.1; -.
DR   EMBL; M83072; AAA58390.1; JOINED.
DR   EMBL; M83073; AAA58390.1; JOINED.
DR   EMBL; M83074; AAA58390.1; JOINED.
DR   PIR; A45803; A45803.
DR   PDB; 1DR9; 10-JAN-01.
DR   SMART; SM00409; IG; 1.
MIM; 112203;
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
KW   Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW   Receptor; 3D-structure.
FT   SIGNAL        1     34
FT   CHAIN        35    288       T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
FT   DOMAIN       35    242       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    243    263       POTENTIAL.
FT   DOMAIN      264    288       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    123       IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN      155    223       IG-LIKE C2-TYPE DOMAIN.
FT   DISULFID     50    116
FT   DISULFID    162    216
FT   CARBOHYD     53     53       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     89     89       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     98     98       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    186    186       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    207    207       N-LINKED (GLCNAC...).
FT   CARBOHYD    211    211       N-LINKED (GLCNAC...).
FT   CARBOHYD    226    226       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    232    232       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   288 AA;  33048 MW;  BA453EE3452B1F4 CRC64;

Query Match             100.0%;  Score 1149;  DB 1;  Length 288;
Best Local Similarity   100.0%;
Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
Pred. No. 3.5e-89;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||||||||||||||||||||||||||||||||
Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
```

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RESULT 2

ID   CD80_RABIT     STANDARD;      PRT;   299 AA.
AC   P42070;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   CD80.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BJ X CHBB:HM;
RX   MEDLINE=95369049; PubMed=7642234;
RA   Isono T., Seto A.;
RT   "Cloning and sequencing of the rabbit gene encoding T-cell
RT   costimulatory molecules.";
RL   Immunogenetics 42:217-220(1995).
CC   -!-  FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
CC        LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
CC        PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
CC        RECEPTOR.
CC   -!-  SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!-  SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!-  SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!-  SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
DR   EMBL; D49843; BAA08643.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
KW   Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW   Receptor.
FT   SIGNAL        1     32
FT   CHAIN        33    299       T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
FT   DOMAIN       33    243       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    244    264       POTENTIAL.
FT   DOMAIN      265    299       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       42    122       IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN      154    222       IG-LIKE C2-TYPE DOMAIN.
FT   DISULFID     49    115
FT   DISULFID    161    215
FT   CARBOHYD     52     52       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     88     88       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     97     97       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    122    122       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    185    185       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    206    206       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    210    210       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   299 AA;  33513 MW;  6744223B5CC91DE0 CRC64;

Query Match              64.2%;  Score 738;  DB 1;  Length 299;
Best Local Similarity    63.9%;
Matches  133;  Conservative   36;  Mismatches   39;  Indels    0;  Gaps    0;
Pred. No. 8.9e-55;

Qy    4 HFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKN 63
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Qy 209 NNHSIVCLIKYGHLRVNQTFNWNTTKQE 211
         ||||:||||||||||||||||||:|||||||
Db 209 NNHSIVCLIKYGELSVSQOIFPWSKPKQE 236

Qy 184 IGHPDPNVKIRCSASGGFPEPRLAWMEDGEELNAVNTTVDQDLDTELYSVSSELDFNVT 208
         |:|:||| |||||||| |||:||:||||||||||||| || |:|||||||:|||||:|
Db 149 FEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMT 183

Db 124 FEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMT 183

Db   89 RTFPDIINNLSLMILALRLSDKGTYTCVVQKNENGSFRREHLTSVILSIRADFPVPSITD 148

Qy   64 RTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISD 123

Db   29 HFSSGLTSQVTSVSKEMAALSCDYNISIDELARMRIYWQKDQQMVLSTISGQVEWPEYKN 88

RESULT 3

CD80_MOUSE

ID   CD80_MOUSE   STANDARD;   PRT;   306 AA.
AC   Q00609;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T lymphocyte activation antigen CD80 precursor (Activation B7-1
DE   antigen) (B7).
GN   CD80 OR B7.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RX   MEDLINE=91341422; PubMed=1714935;
RA   Gray G.S., Freeman G.J., Gimmi C.D., Lombard D.B., Zhou L.J.,
RA   White M., Fingeroth J.D., Gribben J.G., Nadler L.M.;
RT   "Structure, expression, and T cell costimulatory activity of the
RT   murine homologue of the human B lymphocyte activation antigen B7.";
RL   J. Exp. Med. 174:625-631(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93307789; PubMed=7686531;
RA   Selvakumar A., White P.C., Dupont B.;
RT   "Genomic organization of the mouse B-lymphocyte activation antigen
RT   B7.";
RL   Immunogenetics 38:292-295(1993).
CC   -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
CC   LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
CC   PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
CC   RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, GAMMA
CC   INTERFERON STIMULATED MONOCYTES AND NONCIRCULATING B-CELL
CC   MALIGNANCIES.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS POST-
CC   ACTIVATION. PROTEIN WAS MAXIMAL FROM 48 TO 72 HOURS POST-
CC   ACTIVATION. IT'S EXPRESSION WAS MAXIMAL FROM 48 TO 72 HOURS
CC   POST-ACTIVATION.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC   --
CC   --
DR   EMBL; X60958; CAA43291.1; -.
DR   EMBL; L12589; AAA37240.1; ALT_SEQ.
DR   EMBL; L12585; AAA37240.1; JOINED.

DR   EMBL; L12586; AAA37240.1; JOINED.
DR   EMBL; L12587; AAA37240.1; JOINED.
DR   EMBL; L12588; AAA37240.1; JOINED.
DR   PIR; S17291; S17291.
MGD; MGI:101775; CD80.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00410; IG_like; 1.
KW   Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW   Receptor.
FT   SIGNAL   1   37
FT   CHAIN   38   306
FT   DOMAIN   38   246   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   247   268   POTENTIAL.
FT   DOMAIN   269   306   CYTOPLASMIC (POTENTIAL).
FT   DOMAIN   47   126   IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN   158   226   IG-LIKE C2-TYPE DOMAIN.
FT   DISULFID   165   219   POTENTIAL.
FT   DISULFID   54   119   POTENTIAL.
FT   CARBOHYD   93   93   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   149   149   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   99   99   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   189   189   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   210   210   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   214   214   N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   306 AA; 34589 MW; 1DBADE093IB84C62 CRC64;

Query Match   48.8%; Score 561; DB 10; Length 306;
Best Local Similarity   50.7%; Pred. No. 5.9e-40;
Matches 104; Conservative 41; Mismatches 58; Indels   2; Gaps 2;

Qy   12 VTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRTIFDITN 71
         ::|| ||:| |||| | ||| ||||||||:|||| | | :| |||||:|||||:|||
Db   42 LSKSVKDKVLLPCRYNSPHEDESEDRIYWQKHDKVVLSVIAGKLKVWPEVKNRTLYDNT- 100

Qy   72 NLSIVILALRRSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNI 131
         ::| |||||||| | |||| |: ||:|| ||||||||||||||:|||||:|||:|||||
Db 101 TYSLIILGLVLSDRGTYSCVVQKKERGTYEVKHLALVKLSIKADFSTPNITESGNPSADT 160

Qy 132 RRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNISFMCL 191
         |||||| ||||||:|||||||||||:||||:| |||: |||||||||||||:|||:|||
Db 161 KRITCPASGGFPKPRRSWLENGRELPGINTTISQDPESELYTISSQLDFNTTRNHHIKCL 220

Qy 192 IKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||| ||:|| ||||||||| :|:
Db 221 IKYGDAHVSEDFTWEKPPEDP-PDS 244

RESULT 4

CD86_HUMAN

ID   CD86_HUMAN   STANDARD;   PRT;   329 AA.
AC   P42081; Q13655;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T lymphocyte activation antigen CD86 precursor (Activation B7-2
DE   antigen) (CTLA-4 counter-receptor B7.2) (B70) (FUN-1) (BU63).
GN   CD86 OR CD28LG2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94053735; PubMed=7694363;
RA   Freeman G.J., Gribben J.G., Boussiotis V.A., Ng J.W.,
RA   Restivo V.A. Jr., Lombard L.A., Gray G.S., Nadler L.M.;
RT   "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T
RT   cell proliferation.";

```
RL   Science 262:909-911(1993).
RN   [2]
RP   SEQUENCE OF 7-329 FROM N.A.
RX   MEDLINE=94050123; PubMed=7694153;
RA   Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H.,
RA   Lanier L.L., Somoza C.;
RT   "B70 antigen is a second ligand for CTLA-4 and CD28.";
RL   Nature 366:76-79(1993).
RN   [3]
RP   SEQUENCE OF 7-329 FROM N.A.
RC   TISSUE=Foreskin;
RX   MEDLINE=95318831; PubMed=7541777;
RA   Jellis C.L., Wang S.S., Rennert P., Borriello F., Sharpe A.H.,
RA   Green N.R., Gray G.S.;
RT   "Genomic organization of the gene coding for the costimulatory human
RT   B-lymphocyte antigen B7-2 (CD86).";
RL   Immunogenetics 42:85-89(1995).
RN   [4]
RP   CHARACTERIZATION.
RX   MEDLINE=95088403; PubMed=7527824;
RA   Okumura K., Ito D., Azuma M.,
RA   Lanier L.L., O'Fallon S., Phillips J.H., Linsley P.S.;
RT   "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T
RT   cell proliferation, cytokine production, and generation of CTL.";
RL   J. Immunol. 154:97-105(1995).
RN   [5]
RP   IDENTIFICATION AS CD86.
RX   MEDLINE=94348060; PubMed=7520767;
RA   Engel P., Gribben J.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M.,
RA   Nadler L.M., Wakasa H., Tedder T.F.;
RT   "The B7-2 (B70) costimulatory molecule expressed by monocytes and
RT   activated B lymphocytes is the CD86 differentiation antigen.";
RL   Blood 84:1402-1407(1994).
CC   -!-  FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
CC        FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
CC        BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
CC        EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
CC        SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
CC        CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC   -!-  SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!-  TISSUE SPECIFICITY: EXPRESSED BY ACTIVATED B LYMPHOCYTES AND
CC        MONOCYTES.
CC   -!-  SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!-  SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!-  SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC   -!-  DATABASE: NAME=PROW; NOTE=CD guide CD86 entry;
CC        WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd86.htm".
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DR   EMBL; L25259; AAA58389.1; -.
DR   EMBL; U04343; AAB03814.1; -.
DR   EMBL; U17722; AAB86473.1; -.
DR   EMBL; U17717; AAA86473.1; JOINED.
DR   EMBL; U17718; AAA86473.1; JOINED.
DR   EMBL; U17719; AAA86473.1; JOINED.
DR   EMBL; U17721; AAA86473.1; JOINED.
DR   MIM; 601020;
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   SMART; SM00406; IGv; .
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW   Receptor.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    329       T LYMPHOCYTE ACTIVATION ANTIGEN CD86.
FT   DOMAIN       24    247       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    248    268       POTENTIAL.
FT   DOMAIN      269    329       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       33    117       IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN      149    225       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN       40    110       POTENTIAL.
FT   DISULFID    157    218       POTENTIAL.
FT   DISULFID     33     33       ?
FT   CARBOHYD     47     47       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    135    135       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    146    146       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    154    154       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    177    177       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    192    192       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    213    213       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT     27     27       K -> E (IN REF. 3).
SQ   SEQUENCE   329 AA;  37696 MW;  65D4F3826889C87D CRC64;
```

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Query Match             15.8%;  Score 182;  DB 1;  Length 329;
Best Local Similarity   29.0%;  Pred. No. 3.3e-08;
Matches   60;  Conservative   38;  Mismatches   71;  Indels   38;  Gaps   10;

Qy   18  EVATLSC----GHNVSVEELAQTRIYWQKEKKMVLTMM-----SGDMNIWPEYKNRTIFDI   69
             |||        |: ||||  :  ||: ||  ||      | :  |  ||| | |||| ||
Db   34  ETADLPCQFANSQNQSLSELV---VFWQDQENLVLNEVVILGKEKFDSVHSKYMGRTSFD-   89

Qy   70  TNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTS  129
             ::: | |::: | ||  :|| | |   |  |:|  ||:|: :|:  |   |  |: |
Db   90  SDSWTLRLHNLQIRDKGLYQCIIHHKKPTGMIRIHQMNSELSVLANFSQPEI----VPIS  145

Qy  130  NIR-----RIICSTSGGFPEP-HLSWLENGEELNAINTTV-------SQDPETPLYAVS  175
             ||      ||| : |: ||:   | || | || |  | | |       ||   |:
Db  146  NITENVYINLTCSSIHGYPEPKKMSVL----LRFKNSTIEYDGIMQKSQDNVTELYDVS  200

Qy  176  SKLDF---NMTTNHSFMCLIKYGHLRV  199
             |  ||    |:| | | || | |||
Db  201  ISLSVSFPDVTSNMTIFCILETDKTRL  227
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RESULT 5
ICOS_HUMAN

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ID   ICOS_HUMAN     STANDARD;     PRT;     302 AA.
AC   O75144; Q9NRO1; Q9HD18;
DT   15-JUL-1999 (Rel. 38, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   ICOS ligand precursor (B7 homolog 2) (B7-H2)
DE   (B7-related protein-1) (B7RP-1).
GN   ICOSL OR B7H2 OR B7RP1 OR KIAA0653.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Dendritic cell;
RX   MEDLINE=20477846; PubMed=11023515;
RA   Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.;
RT   "Costimulation of T cells by B7-H2, a B7-like molecule that binds
RT   ICOS.";
RL   Blood 96:2808-2813(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC   TISSUE=Peripheral blood lymphocytes;
RX   MEDLINE=20465019; PubMed=11007762;
RA   Yoshinaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner K.,
RA   Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H.,
RA   Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.;
RT   "Characterization of a new human B7-related protein: B7RP-1 is the
RT   ligand to the co-stimulatory protein ICOS.";
RT   Int. Immunol. 12:1439-1447(2000).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Leukocyte;
```

```
RX   MEDLINE=20126021; PubMed=10657606;
RA   Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A.,
RA   Leonard J.P., Hunter S.E., Zollner R., Thomas J.L., Miyashiro J.S.,
RA   Jacobs K.A., Collins M.;
RT   "Identification of GL50, a novel B7-like protein that functionally
RT   binds to ICOS receptor.";
RL   J. Immunol. 164:1653-1657(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98403880; PubMed=9734811;
RA   Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
RA   Kotani H., Nomura N., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. X.
RT   The complete sequences of 100 new cDNA clones from brain which can
RT   code for large proteins in vitro.";
RL   DNA Res. 5:169-176(1998).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RA   Ling V., Dunussi-Joannopoulos K.;
RT   "GL50 molecules and uses therefor.";
RL   Patent number WO0121796, 29-MAR-2001.
CC   -!- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
CC       ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
CC       CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
CC       DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
CC       MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
CC       WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
CC       STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2;
CC       ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART,
CC       KIDNEY, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE
CC       MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUKOCYTES,
CC       SPLEEN, THYMUS AND TONSIL), WHILE ISOFORM 2 IS DETECTED ONLY IN
CC       LYMPH NODES, LEUKOCYTES AND SPLEEN.
CC   -!- INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY
CC       TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND
CC       MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC       SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- CAUTION: Ref.4 sequence differs from that shown in position 300
CC       onward for an unknown reason.
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DR   EMBL; AF199028; AAF34739.1; -.
DR   EMBL; AF289028; AAG01176.1; -.
DR   EMBL; AF216749; AAK16241.1; -.
DR   EMBL; AB014553; BAA31628.1; ALT_SEQ.
DR   EMBL; AX100599; CAC36465.1; -.
DR   MIM; 605717;
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
KW   B-cell activation; IG-like; 1.
KW   Immunoglobulin domain; Immune response; Glycoprotein;
KW   Alternative splicing.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    302       ICOS LIGAND.
FT   DOMAIN       19    256       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    257    277       POTENTIAL.
FT   DOMAIN      278    302       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       30    120       IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN      151    223       IG-LIKE C2-TYPE DOMAIN.
FT   DISULFID     37    113       POTENTIAL.
FT   DISULFID    158    216       POTENTIAL.
FT   CARBOHYD     70     70       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    137    137       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    173    173       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    186    186       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    225    225       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARSPLIC    300    302       GHV -> ESWNLLLLS (IN ISOFORM 2).
SQ   SEQUENCE   302 AA;  33349 MW;  647934E21B55E34A CRC64;

Query Match             14.0%;  Score 161;  DB 1;  Length 302;
  Best Local Similarity   26.4%;
  Matches   57;  Conservative   36;  Mismatches   95;  Indels   28;  Gaps    8;

Qy         14 KEVKEV-----ATLSCG--HNVSVEELAQTRIYWQ-KEKKMVLT----MMSGDMNIWPEYKN 63
              |||:|:     ||:|       || || || ||   ||: ||       || ||| ||| :
Db         23 KEVRAMGSDVELSCACPEGGSRFDLNDVYVVWQTSESKTVTYHIPQNSSLENVDSRYRN 82

Qy         64 RTIFD---ITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVILSVKADFPTP 119
              | :        |:| |:| |  || :|| | :  |    |  ||:| | | |  | :||
Db         83 RALMSBPAGMLRGDFSLRLFNVTPQDEQKFHCLVLS-QSLGFQEVLSVEVTLHVAANFSVP 141

Qy        120 SISDFEIPTSNIRIRICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETE-------L 171
              :::   | | | : ||||:|| |||| |:|: || | :| |:: |  ||          |
Db        142 VVSAPHSPSQDELTFTCTSINGYPRPNVVWINKTD----NSLLDQALQNDTVFLNMRGL 196

Qy        172 YAVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNT 207
              | :  |:  ||: |  : ||:|   | :||     |
Db        197 YDVVSVLRIARPSVNIGCCIENVLLQQNLIVGSQT 232
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RESULT 6
ID   CD86_MOUSE     STANDARD;      PRT;   309 AA.
AC   P42082;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T lymphocyte activation antigen CD86 precursor (Activation B7-2
DE   antigen) (Early T cell costimulatory molecule-1) (ETC-1).
GN   CD86.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129;
RX   MEDLINE=96094437; PubMed=7499829;
RA   Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;
RT   "Differential expression of alternate mB7-2 transcripts.";
RL   J. Immunol. 155:5490-5497(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94065585; PubMed=7504059;
RA   Freeman G.J., Borriello F., Hodes R.J., Reiser H., Gribben J.G.,
RA   Ng J.W., Kim J., Goldberg J.M., Hathcock K., Laszlo G., Lombard L.A.,
RA   Wang S., Gray G.S., Nadler L.M., Sharpe A.H.;
RT   "Murine B7-2, an alternative CTLA4 counter-receptor that costimulates
RT   T cell proliferation and interleukin 2 production.";
RL   J. Exp. Med. 178:2185-2192(1993).
RN   [3]
RP   SEQUENCE OF 7-309 FROM N.A.
RX   MEDLINE=94309971; PubMed=7513726;
RA   Chen C., Gault A., Shen L., Nabavi N.;
RT   "Molecular cloning and expression of early T cell costimulatory
RT   molecule-1 and its characterization as B7-2 molecule.";
RL   J. Immunol. 152:4929-4936(1994).
CC   -!- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
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CC       FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
CC       BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
CC       EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
CC       SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
CC       CELLS, WITHIN 24 HOURS AFTER ACTIVATION.
CC  -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS.
CC  -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC  -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC  -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC  -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-7 IS THE INITIATOR.
CC  ---------------------------------------------------------------------------
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  ---------------------------------------------------------------------------
DR  EMBL; L25606; AAA79770.1; -.
DR  EMBL; U39456; AAC52334.1; -.
DR  EMBL; U39455; AAC52334.1; -.
DR  EMBL; U39459; AAC52334.1; ALT_INIT.
DR  EMBL; U39461; AAC52336.1; JOINED.
DR  EMBL; U39462; AAC52336.1; JOINED.
DR  EMBL; U39463; AAC52336.1; JOINED.
DR  EMBL; U39464; AAC52334.1; JOINED.
DR  EMBL; U39465; AAC52336.1; JOINED.
DR  EMBL; U39466; AAC52336.1; JOINED.
DR  EMBL; S70108; AAB30744.2; ALT_INIT.
DR  MGD; MGI:101773; Cd86.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  SMART; SM00406; IGv; 1.
DR  PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW  Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW  Receptor.
FT  SIGNAL        1     23
FT  CHAIN        24    309       T LYMPHOCYTE ACTIVATION ANTIGEN CD86.
FT  DOMAIN       24    244       EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM    245    265       POTENTIAL.
FT  DOMAIN      266    309       CYTOPLASMIC (POTENTIAL).
FT  DOMAIN       33    117       IG-LIKE V-TYPE DOMAIN.
FT  DOMAIN      149    223       IG-LIKE C2-TYPE DOMAIN.
FT  DISULFID     40    110       POTENTIAL.
FT  DISULFID    157    216       POTENTIAL.
FT  CARBOHYD     33     33       N-LINKED (GLCNAC).    (POTENTIAL).
FT  CARBOHYD     47     47       N-LINKED (GLCNAC).    (POTENTIAL).
FT  CARBOHYD     92     92       N-LINKED (GLCNAC).    (POTENTIAL).
FT  CARBOHYD    135    135       N-LINKED (GLCNAC).    (POTENTIAL).
FT  CARBOHYD    146    146       N-LINKED (GLCNAC).    (POTENTIAL).
FT  CARBOHYD    154    154       N-LINKED (GLCNAC).    (POTENTIAL).
FT  CARBOHYD    175    175       N-LINKED (GLCNAC).    (POTENTIAL).
FT  CARBOHYD    190    190       N-LINKED (GLCNAC).    (POTENTIAL).
FT  CARBOHYD    231    231       N-LINKED (GLCNAC).    (POTENTIAL).
SQ  SEQUENCE    309 AA;   34665 MW;  8F58DCD1FB81D5EA CRC64;

Query Match             13.2%;
Best Local Similarity   26.18%;
Matches    52;  Conservative  43;  Mismatches  78;  Indels  26;  Gaps  10;  Score 152;  DB 1;  Length 309;

Qy    20  ATLSC---------GHNVSVEELAQTRIYWQKEKKMVL--------TMMSGDMNIWPEYKNRIFDI  69
          | |:|       || |:||          ||  | ||| ||
Db    36  AYLPCPFTRAQNISLSELV---VFWQDQQKLVLYEHYLGTEKLDSVN-AKYLGRTSFD-  89

Qy    70  TNNLSIVILALRPSDEGTYECVVLKYEK----DAFKREHLAEVTLSVKADFPTPSISDFEIP  127
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Db    90  RNNWTLRIHNVQIKDMGSYDCFIQKKPPTGSIILQQTLTE--LSVIANFSEPEIKLAQNV  147
Qy   128  TSNIR-RIICSTSGGFPEPHLSW--LENGEELNAINTTVSQDPETELYAVSSKLDFNM--  182
Db   148  TGNSGINLTCTSKQGHPKPKKMYFLITNSTNEYGDMNQISQDNVTELFFSISNSLSLSFPD  207
Qy   183  -TTNHSFMCLIKYGHLRVN  200
Db   208  GVWHMTVCVLETESMKIS  226

RESULT 7
ICOL_MOUSE

ID   ICOL_MOUSE     STANDARD;      PRT;    322 AA.
AC   Q9JHJ8;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein G150)
DE   (B7-related protein-1) (B7RP-1) (LICOS)
GN   ICOSL OR B7H2 OR B7RP1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC   TISSUE=Lymphocytes;
RX   MEDLINE=20083495; PubMed=10617205;
RA   Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmiento U., Guo J.,
RA   Horan T., Shih G., Zhang M., Coccia M.A., Kohno T., Tafuri-Bladt A.,
RA   Brankow D., Campbell P., Chang D., Chiu L., Dai T., Duncan G.,
RA   Elliott G.S., Hui A., McCabe S.M., Scully S., Shahinian A.,
RA   Shaklee C.L., Van G., Mak T.W., Senaldi G.;
RT   "T-cell co-stimulation through B7RP-1 and ICOS.";
RL   Nature 402:827-832(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Thymus;
RX   MEDLINE=20015817; PubMed=10549624;
RA   Swallow M.M., Wallin J.J., Sha W.C.;
RT   "B7h, a novel costimulatory homolog of B7.1 and B7.2, is induced by
RT   TNFalpha.";
RL   Immunity 11:423-432(1999).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   STRAIN=C3H/HeJ; TISSUE=Fetal thymus;
RX   MEDLINE=20126021; PubMed=10657606;
RA   Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A.,
RA   Leonard J.P., Hunter S.E., Zollner R., Thomas J.L., Miyashiro J.S.,
RA   Jacobs K.A., Collins M.;
RT   "Identification of GL50, a novel B7-like protein that functionally
RT   binds to ICOS receptor.";
RL   J. Immunol. 164:1653-1657(2000).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Peripheral blood lymphocytes;
RX   MEDLINE=21286479; PubMed=11390480;
RA   Ling V., Wu P.W., Miyashiro J.S., Marusic S., Finnerty H.F.,
RA   Collins M.;
RT   "Differential expression of inducible costimulator-ligand splice
RT   variants: lymphoid regulation of mouse gl50-b and human gl50
RT   molecules.";
RL   J. Immunol. 166:7300-7308(2001).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA   Ling V., Dunussi-Joannopoulos K.;
RT   "GL50 molecules and uses therefor.";
RL   Patent number WO0121796, 29-MAR-2001.
CC   -!- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
CC   ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
CC   CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
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CC DIFFERENTIATION INTO PLASMA CELLS, COULD PLAY AN IMPORTANT ROLE IN
CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
CC STIMULATING MEMORY T CELL FUNCTION. DURING PREGNANCY, MAY FUNCTION
CC TO SKEW THE CYTOKINE OF MATERNAL T-CELLS TOWARD IMMUNOPROTECTIVE
CC TH2 PHENOTYPE.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2/B;
CC   ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: ISOFORM 1 HIGHEST EXPRESSION IN LYMPHOID
CC   TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NODES
CC   (PARTICULARLY IN THE CORTEX AND IN BOTH PRIMARY AND SECONDARY
CC   FOLLICLES), THYMUS (PREDOMINANTLY IN THE MEDULLA) AND PEYER'S
CC   PATCHES (MOSTLY IN THE FOLLICLES), LOWER LEVELS IN MANY
CC   NONLYMPHOID TISSUES, SUCH AS BRAIN, HEART, KIDNEY, LIVER, LUNG,
CC   SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC B-
CC   CELLS, T-CELLS, DENDRITIC CELLS AND MACROPHAGES. THE EXPRESSION OF
CC   ISOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY.
CC -!- DEVELOPMENTAL STAGE: DETECTED EARLY IN HEMOPOIESIS: IN THE YOLK
CC   SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER AT
CC   14.5 DPC.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC   SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC ---

DR EMBL; AF216747; AAF45149.1; -.
DR EMBL; AF199027; AAF34738.1; -.
DR EMBL; AX100591; CAC36463.1; -.
DR EMBL; AX100593; CAC36464.1; -.
DR EMBL; AF394451; AAK77544.1; -.
DR MGD; MGI:1354701; Icosl.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG_like; 1.
KW B-cell activation; Immune response; Glycoprotein; Signal; Transmembrane; Multigene family;
KW Alternative splicing.
FT SIGNAL   1   46
FT CHAIN   47   322   BY SIMILARITY.
FT DOMAIN   47   277   ICOS LIGAND.
FT TRANSMEM   278   298   EXTRACELLULAR (POTENTIAL).
FT DOMAIN   299   322   POTENTIAL.
FT DOMAIN   55   145   CYTOPLASMIC (POTENTIAL).
FT DOMAIN   178   250   IG-LIKE V-TYPE DOMAIN.
FT DOMAIN   31   38   IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN   289   292   POLY-LEU.
FT DOMAIN   62   138   POLY-ALA.
FT DISULFID   185   243   POTENTIAL.
FT CARBOHYD   71   71   N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD   120   120   N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD   163   163   N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD   200   200   N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD   213   213   N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD   252   252   N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD   255   265   N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD   321   322   HA -> TWAPVPYQDYLIPRYLMSPCLKTRGLP (IN
FT VARSPLIC   ISOFORM 2).
FT CONFLICT   237   237   R -> H (IN REF. 4 AND 5; CAC36464).
SQ SEQUENCE   322 AA; 35960 MW; 55CCBA4AD12E47E6 CRC64;

Query Match 13.1%; Score 150.5; DB 1; Length 322;

RESULT 8

ID   CD86_RABIT   STANDARD;   PRT;   330 AA.
AC   P42071;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   CD86.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B/J X CHBB:HM;
RX   MEDLINE=95369849; PubMed=7642234;
RA   Isono T., Seto A.;
RT   "Cloning and sequencing of the rabbit gene encoding T-cell
RT   costimulatory molecules.";
RL   Immunogenetics 42:217-220(1995).
CC -!- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
CC   FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
CC   BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
CC   EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
CC   SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
CC   CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC ---

DR EMBL; D49842; BAA08642.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor.
FT SIGNAL   1   22   POTENTIAL.
FT CHAIN   23   330
FT DOMAIN   23   247   EXTRACELLULAR (POTENTIAL).
FT TRANSMEM   248   268   POTENTIAL.
FT DOMAIN   269   330   CYTOPLASMIC (POTENTIAL).

Best Local Similarity 27.1%; Pred. No. 1.4e-05;
Matches 65; Conservative 32; Mismatches 102; Indels 41; Gaps 12;

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Qy    2  LSHFC--SGVIHVTKEVKEVATLSCGHNVSVE------ELAQTRIYWQKEKKMV-----L   48
            ||  |                   |           |  |||:|| ||||       |
Db   38  LSSLCAASAETEVGAMVGSNVVLSC-----IDPHRHFNLSGLYVWQIENPEVSVTYYL   92

Qy   49  TMMSGDMNIWPEYKNRTIFDITN----NLSIVILALRPSDEGTYECVVLKYEKDAFKREH  104
            |           |  |        |          |:|| || || |
Db   93  PYKSPGINVDSSYKNRGHLSLDSMKQGNFSLYLKNVTPQDQEEFTCRV--FMNTAFELVK  150

Qy  105  LAE--VTLSVKADFPTP--SISDFEIPTSNIRRICSTSGGFPEPHLSWLENGEELNAIN   160
            |      |       ||         :  |  |||:|| ||||||| |
Db  151  ILEEVVRLRVAANFSTPVISTSDSSSNPGQE-RTYICMSKNGYPEPNLYWI-NTTDNSLID  208

Qy  161  TTVSQDP-----ETELYAVSSKLDFNMTTNHSFMCLLKYGHLRVN------QTFNWNTTK   209
            ||:|        |  |     |       |  |||     |          |||| |||
Db  209  TALQNNTVYLNKLGLYDVISTLRLPWTSRGDVLCCVENVALHQNITSISQAESFTGNNTK  268
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RESULT 9

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C166_MOUSE

ID   C166_MOUSE     STANDARD;      PRT;    583 AA.
AC   Q61490; O70136;
DT   01-NOV-1997 (Rel. 35, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   CD166 antigen precursor (Activated leukocyte-cell adhesion molecule)
DE   (ALCAM) (DM-GRASP protein).
GN   ALCAM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=Brain;
RX   MEDLINE=94376084; PubMed=8089660;
RA   Kanki J.P., Chang S., Kuwada J.Y.;
RT   "The molecular cloning and characterization of potential chick
RT   DM-GRASP homologs in zebrafish and mouse.";
RL   J. Neurobiol. 25:831-845(1994).
RN   [2]
RP   SEQUENCE OF 227-583 FROM N.A.
RC   STRAIN=NFS;
RX   MEDLINE=97353242; PubMed=9209500;
RA   Bowen M.A., Bajorath J., D'Egidio M., Whitney G.S., Palmer D.,
RA   Kobarg J., Starling G.C., Siadak A.W., Aruffo A.;
RT   "Characterization of mouse ALCAM (CD166): the CD6 binding domain is
RT   conserved in different homologs and mediates cross-species binding.";
RL   Eur. J. Immunol. 27:1469-1478(1997).
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DR   EMBL; U95030; AAC06342.1; -.
DR   EMBL; L25274; AAA37528.1; -.
DR   MGD; MGI:1313266; Alcam.
DR   HSSP; Q13740; 1KJC.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00410; IG_like; 2.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW   Repeat; Signal.
FT   SIGNAL         1     27
FT   CHAIN         28    583    POTENTIAL.
FT   DOMAIN        28           CD166 ANTIGEN.
FT   DOMAIN        28    527    EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     528    549    POTENTIAL.
FT   DOMAIN       550    583    CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       263    321    IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN       347    399    IG-LIKE C2-TYPE DOMAIN 2.
FT   DOMAIN       428    492    IG-LIKE C2-TYPE DOMAIN 3.
FT   DISULFID      43    113    POTENTIAL.
FT   DISULFID     157    220    POTENTIAL.
FT   DISULFID     270    313    POTENTIAL.
FT   DISULFID     354    392    POTENTIAL.
FT   DISULFID     435    485    POTENTIAL.
FT   CARBOHYD      95     95    N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     167    167    N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     265    265    N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     306    306    N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     361    361    N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     457    457    N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     480    480    N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     499    499    N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT     227    227    S -> F (IN REF. 2).
FT   CONFLICT     232    232    PSGQKT -> AAGIPA (IN REF. 2).
FT   CONFLICT     454    454    S -> F (IN REF. 2).
SQ   SEQUENCE     583 AA;  65161 MW;  E7BAFA8FCABF9489 CRC64;
```

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Query Match             11.7%;  Score 134.5;  DB 1;  Length 583;
Best Local Similarity   25.2%;
  Matches   38;  Conservative   34;  Mismatches   54;  Indels   25;  Gaps   7;

Qy     59  PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPT  118
           |||| :|  ||||||  | :| ||:||||    | |:|  | ::| |:|:||||:||||  |
Db     84  PEYKDR--LSLSENYTLSIANAKISDEKRFVCMLVT-EDNVFEAPTLVKV------FKQ  133

Qy    119  PSISDFE-----IPTSNIRRI-ICSTSGGFPEPHLSWLENGEELNAINTTTVS------QD  166
           |:|   :|       | || |  ::|| : || :||:|||  :|| |   |          |
Db    134  PSKPEIVNKAPFLETDQLKKLGDCISRDSYPDGNITWYRNGKVLQPVEGEVAIIFKKEID  193

Qy    167  PETELYAVSSKLDFNMTTNH---SFMCLIKY  194
           | | | ||:| : | :|  | |   :| || |
Db    194  PGTQLYTVTSLSLEYKJTRSDIQMPFTCSVTY  224
```

RESULT 10

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C166_HUMAN

ID   C166_HUMAN     STANDARD;      PRT;    583 AA.
AC   Q13740; O60892;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
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Qy     18  EVATLSCGH-NVSVEELAQTRIYWQKEKKMVLIMM----SGDMNIWPEYKNRTIFDITN-  71
               ::|:|    |:||| ||:|:||  :     :|||   |  :| :|   | :|:| |
Db     34  KTADLPCQFTNSQSRSLSELVWFWQDQERLVLYELFLGREKPDNVDPKYIGRTSFDQESW  93

Qy     72  NLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPFTPSISDFELPTSNI  131
               ||||  |   :  ::|:  :::||  |    :||:||  |::  | :   || |  |  |
Db     94  NLQIHNVQIK--DKGVYQCFVHHRGAKGLVPIYQMNSELSVLANFTQPEIT---LISNI  147

Qy    132  RR------IICSTSGGFPEPHLSWLENGEELNAINTTTV--------SQDPETELY--AVSS  176
                        ||:|| ||| :||:||| :||     | |||         | ||| |  ::
Db    148  TRNSAINLTCSSVQGYPEPKKMFF----VLKIENATTEYDGVIEKSQDNVTGLYNISISG  203

Qy    177  KLDF-NMTTNHSFMCLIKYGHLRVNQIFNWNTTKQEHPP  214
               ||:|  |:   |:|| ||:      |:|        |:::|:|
Db    204  SITFSDDIRNAIIYCVL-------QTESTEIYSQ-HFP  233
```

```
DE   CD166 antigen precursor (Activated leukocyte-cell adhesion molecule)
DE   (ALCAM).
GN   ALCAM OR MEMD.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95279947; PubMed=7760007;
RA   Bowen M.A., Patel D.D., Li X., Modrell B., Malacko A.R.,
RA   Wang W.-C., Marquardt H., Neubauer M., Pesando J.M., Francke U.,
RA   Haynes B.F., Aruffo A.;
RT   "Cloning, mapping, and characterization of activated leukocyte-cell
RT   adhesion molecule (ALCAM), a CD6 ligand.";
RL   J. Exp. Med. 181:2213-2220(1995).
RN   [2]
RP   SEQUENCE OF 2-583 FROM N.A.
RX   MEDLINE=98161527; PubMed=9502422;
RA   Degen W.G., van Kempen L.C., Gijzen E.G., van Groningen J.J.,
RA   van Kooyk Y., Bloemers H.P., Swart G.W.;
RT   "MEMD, a new cell adhesion molecule in metastasizing human melanoma
RT   cell lines, is identical to ALCAM (activated leukocyte cell adhesion
RT   molecule).";
RL   Am. J. Pathol. 152:805-813(1998).
RN   [3]
RP   3D-STRUCTURE MODELING OF 28-133.
RX   MEDLINE=96050095; PubMed=8520490;
RA   Bajorath J., Bowen M.A., Aruffo A.;
RT   "Molecular model of the N-terminal receptor-binding domain of the
RT   human CD6 ligand ALCAM.";
RL   Protein Sci. 4:1644-1647(1995).
CC   -!- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN
CC       NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC
CC       INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO
CC       ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF
CC       THE NERVOUS SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD166 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd166.htm".
```

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DR   EMBL; L38608; AAB59499.1; -.
DR   EMBL; Y10183; CAA71256.1; -.
DR   PDB; 1KJC; 03-APR-96.
DR   MIM; 601662;
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00410; IG_like; 2.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   Cell adhesion; Signal; 3D-structure; Polymorphism.
KW   Repeat; Signal; Immunoglobulin domain; Glycoprotein; Transmembrane;
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FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28    583       CD166 ANTIGEN.
FT   DOMAIN       28    527       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    528    549       POTENTIAL.
FT   DOMAIN      550    583       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       36    120       IG-LIKE V-TYPE DOMAIN 1.
FT   DOMAIN      150    227       IG-LIKE V-TYPE DOMAIN 2.
FT   DOMAIN      263    321       IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN      347    399       IG-LIKE C2-TYPE DOMAIN 2.
FT   DOMAIN      428    492       IG-LIKE C2-TYPE DOMAIN 3.
FT   DISULFID     43    113       POTENTIAL.
FT   DISULFID    157    220       POTENTIAL.
FT   DISULFID    270    313       POTENTIAL.
FT   DISULFID    354    392       POTENTIAL.
FT   DISULFID    435    485       POTENTIAL.
FT   CARBOHYD     91     91       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     95     95       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    167    167       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    265    265       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    306    306       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    361    361       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    457    457       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    480    480       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    499    499       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARIANT     258    258       N -> S.
FT   VARIANT     301    301       M -> T.
FT                               /FTId=VAR_003908.
FT   VARIANT     301    301       M -> T.
FT                               /FTId=VAR_003907.
SQ   SEQUENCE   583 AA;  65132 MW;  E023FB3974A60284 CRC64;
```

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Qy              59 PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLRYEKDAFKREHLAEVTLSVKRADFPT 118
                   ||| || |||| |:|| |  |  :| :|  :| : |::|  | ::|||   : ::|   |
Db              84 PEYKDR--LNLSENYTLSISNARISDEKRFVCMLVT-EDNVFEAPITVKV-------FKQ 133

Qy             119 PSISDFE-----IPTSNIRRI-ICSTSGGFPEPHLSWLENGEELNAINTTV------SQD 166
                   || |:| |      |:|  |: ||:|:| | :|| : : |:| |         ||
Db             134 PSKPEIVSKALFLETEQLKKILGDCISEDSYPDGNITWYRNGKVLIHPLEGAVVIIFKKEMD 193

Qy             167 PETELELYAVSSKLDFNMT---TNHSFMCLIKY 194
                   | |:| | :|: |::| |     | |:  :|
Db             194 PVTQLYTMTSLEYKYTKADIQMPFTCSVTY 224
```

Query Match 11.6%; Score 133.5; DB 1; Length 583;
Best Local Similarity 24.5%;
Matches 37; Conservative 35; Mismatches 54; Indels 25; Gaps 7;

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RESULT 11
ID   BRF1_EBV     STANDARD;      PRT;   221 AA.
AC   P03228;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   33 kDa early protein (p33).
GN   BARF1.
OS   Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Gammaherpesvirinae; Lymphocryptovirus.
OX   NCBI_TaxID=10377;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84270667; PubMed=6087149;
RA   Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA   Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
RA   Tuffnell P.S., Barrell B.G.;
RT   "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL   Nature 310:207-211(1984).
RN   [2]
RP   IDENTIFICATION OF PROTEIN.
RX   MEDLINE=90059873; PubMed=2555151;
RA   Wei M.X., Ooka T.;
RT   "A transforming function of the BARF1 gene encoded by Epstein-Barr
```

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RT   virus.";
RL   EMBO J. 8:2897-2903(1989).
CC   -!- FUNCTION: BARF1 HAS TRANSFORMING ACTIVITY.
CC   --------------------------------------------------------------------------
```

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DR   EMBL; V01555; CAA24809.1; -.
DR   PIR; A03792; QQBE48.
DR   PIR; S33058; S33058.
DR   InterPro; IPR003600; Ig_like.
DR   SMART; SM00410; IG_like; 1.
KW   Early protein; Oncogene.
SQ   SEQUENCE   221 AA;  24471 MW;  CA5A24D1EA2875BE CRC64;

Query Match             11.2%;  Score 129;  DB 1;  Length 221;
Best Local Similarity   27.0%;  Pred. No. 0.00055;
Matches   43;  Conservative  25;  Mismatches  47;  Indels  44;  Gaps   8;

Qy   18  EVATLSCGHNVSVEELAQTRIYWQK-----EKKMVLTMMSGDMNIWPE   60
             ::  : :  : :: :  :  :     ||::| :::| :|: | |
Db   19  QAVTAFLGERVTLYS-----YWRRVSLGPEIEVSWFKLGPGEQVLIGRMHHDV-IFIE   71

Qy   61  YKNRTIFDI---TNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEV---TLSV--  112
             | |   |      || :| :  :| ||:| || ::   ::  ::  :         :|
Db   72  WPFRGFPFDIHRSANTFLVTAANISHDGNYLCRMKLGEIEVTKQEHLSVVKPLTLSVHS  131

Qy  113  -KADFPPSISDEIPISNIRRIICSTSGFPEPHISWL              150
              | | |  |    :  :| : ||         | |
Db  132  ERSQFP-------DFSVLT------VTCTVNAFPHPHVQWL         159
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RESULT 12
ID   BUTY_HUMAN     STANDARD;      PRT;   526 AA.
AC   Q13410;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Butyrophilin precursor (BT).
GN   BTN1A1 OR BTN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast;
RX   MEDLINE=96201696; PubMed=8611614;
RA   Taylor M.R., Peterson J.A., Ceriani R.L., Couto J.R.;
RT   "Cloning and sequence analysis of human butyrophilin reveals a
RT   potential receptor function.";
RL   Biochim. Biophys. Acta 1306:1-4(1996).
CC   -!- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
CC       MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
CC       ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
CC       MEMBRANE (BY SIMILARITY).
CC   -!- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
CC       (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC       SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC   --------------------------------------------------------------------------
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DR   EMBL; U39576; AAC50489.1; -.
DR   MIM; 601610; -.
DR   InterPro; IPR001870; Gamma_carboxylse.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   InterPro; IPR003597; SPRY.
DR   InterPro; IPR003878; SPRY_domain.
DR   Pfam; PF00047; Ig; 1.
DR   Pfam; PF00622; SPRY; 1.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00449; SPRY; 1.
FT   SIGNAL        1     26
FT   CHAIN        27    526       BUTYROPHILIN.
FT   DOMAIN       27    242       BY SIMILARITY.
FT   TRANSMEM    243    269       POTENTIAL.
FT   DOMAIN      270    526       EXTRACELLULAR (POTENTIAL).
FT                                CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     55     55       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    215    215       N-LINKED (GLCNAC...) (POTENTIAL).
KW   Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
SQ   SEQUENCE   526 AA;  59004 MW;  E9ECA0CF8DAF94D5 CRC64;

Query Match             11.8%;  Score 127;  DB 1;  Length 526;
Best Local Similarity   27.5%;  Pred. No. 0.0024;
Matches   52;  Conservative  33;  Mismatches  84;  Indels  20;  Gaps  10;

Qy   16  VKEVATLSC--GHNVSVEELAQTRIYWQKEKKMVLTMMSG---DMNIWPEYKNRTIF---   67
             | :  |      ||: :| :  ||| |:  ::  :|       :|:  | |
Db   42  VGEDAELPCRLSPNASAEHL-ELRWFRKKVSPAVLVHRDGREQEARQMPEYRGRATLVQD  100

Qy   68  -DITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKRADFPTPSISDFEI  126
             : | :: :|  |  :: |: | |      ::   :   :  :|    : |
Db  101  GIAKGRVALRIRGVRVSDDGEYTCF---FREDGSYEEAL--VHLKVAALGSDPHIS-MQV   154

Qy  127  PTSNIRRIICSTSGFPEPHISW-LENGEELNAINTTVSODPETE-LYAVSSKLDFNMTT    184
             | :  | ::   |||  :|    ::: :    |  : :   :    |
Db  155  QENGEICLECTSVGWYPEPQVQWRTSKGEKFP--STSESRNPDEEGLFTVAASVIIRDTS  212

Qy  185  NHSFMCLIK              193
             |:  :|
Db  213  TKNVSCYIQ              221
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RESULT 13
ID   C166_CHICK     STANDARD;      PRT;   588 AA.
AC   P42292;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   CD166 antigen precursor (SC1 glycoprotein) (BEN glycoprotein) (DM-
DE   GRASP protein) (JC7 protein).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 34-53.
RC   TISSUE=Embryo;
RX   MEDLINE=92030150; PubMed=1931049;
RA   Tanaka H., Matsui T., Agata A., Tomura M., Kubota I.,
RA   McFarland K.C., Kohr B., Lee A., Phillips H.S., Shelton D.L.;
RT   "Molecular cloning and expression of a novel adhesion molecule, SC1.";
RL   Neuron 7:535-545(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91337449; PubMed=1873027;
RA   Burns F.R., von Kannen S., Guy L., Raper J.A., Kamholz J.,
RA   Chang S.;
```

RT   "DM-GRASP, a novel immunoglobulin superfamily axonal surface protein
RT   that supports neurite extension.";
RL   Neuron 7:209-220(1991).
RN   [3]
RP   SEQUENCE FROM N.A. AND SEQUENCE OF 34-52; 87-93; 504-512 AND 569-582.
RC   TISSUE=Bursa of fabricius;
RX   MEDLINE=92302224; PubMed=1608932;
RA   Pourquie O., Corbel C., le Caer J.-P., Rossier J., le Douarin N.M.;
RT   "BEN, a surface glycoprotein of the immunoglobulin superfamily, is
RT   expressed in a variety of developing systems.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:5261-5265(1992).
RN   [4]
RP   POSSIBLE FUNCTION.
RX   MEDLINE=92211411; PubMed=1313497;
RA   Pourquie O., Hallonet M.E.R., le Douarin N.M.;
RT   "Association of BEN glycoprotein expression with climbing fiber
RT   axonogenesis in the avian cerebellum.";
RL   J. Neurosci. 12:1548-1557(1992).
CC   -!- FUNCTION: HOMOPHILIC ADHESION MOLECULE ASSOCIATED WITH CLIMBING
CC   FIBER AXONOGENESIS. SUPPORTS NEURITE EXTENSION.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A RESTRICTED POPULATION OF AXONS.
CC   WITHIN THE SPINAL CORD IT IS LOCALIZED TO AXONS IN THE DORSAL
CC   FUNICULUS, MIDLINE FLOOR PLATE CELLS, AND MOTONEURONS. FOUND IN
CC   EPITHELIA, CENTRAL NERVOUS SYSTEM, AND HEMOPOIETIC CELLS. EACH
CC   DEVELOPING SYSTEM CARRIES DIFFERENTLY GLYCOSYLATED MOLECULAR FORMS
CC   OF BEN.
CC   -!- DEVELOPMENTAL STAGE: WIDELY EXPRESSED DURING EMBRYONIC
CC   DEVELOPMENT.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.

DR   EMBL; S63276; AAB20170.1; -.
DR   EMBL; M76678; AAA48602.1; -.
DR   EMBL; X64301; CAA45579.1; -.
DR   HSSP; Q13740; 1KCC.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; Ig; 5.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00410; IG_like; 2.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW   Repeat; Signal.
FT   SIGNAL   1   33
FT   CHAIN   34   588   CD166 ANTIGEN.
FT   DOMAIN   34   532   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   533   553   POTENTIAL.
FT   DOMAIN   554   588   CYTOPLASMIC (POTENTIAL).
FT   DOMAIN   42   126   IG-LIKE V-TYPE DOMAIN 1.
FT   DOMAIN   156   233   IG-LIKE V-TYPE DOMAIN 2.
FT   DOMAIN   269   326   IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN   352   404   IG-LIKE C2-TYPE DOMAIN 2.
FT   DOMAIN   433   497   IG-LIKE C2-TYPE DOMAIN 3.
FT   DISULFID   49   119
FT   DISULFID   163   226
FT   DISULFID   276   319
FT   DISULFID   359   397
FT   DISULFID   440   490
FT   CARBOHYD   42   42   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   101   101   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   173   173   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   199   199   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   271   271   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   312   312   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   366   366   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   462   462   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   485   485   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   504   504   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT   2   10   MEPPAAAAR -> EPPSRRRP (IN REF. 3).
FT   CONFLICT   25   25   A -> S (IN REF. 3).
FT   CONFLICT   112   113   SD -> RH (IN REF. 3).
FT   CONFLICT   329   329   A -> T (IN REF. 2).
FT   CONFLICT   401   402   LQ -> HK (IN REF. 2).
SQ   SEQUENCE   588 AA; 65726 MW; 2A28612D0164531E CRC64;

Query Match   10.7%; Score 122.5; DB 1; Length 588;
Best Local Similarity   25.7%; Pred. No. 0.0064;
Matches   39; Conservative   32; Mismatches   54; Indels   27; Gaps   8;

Qy   59 PEYKNRTIFDITTNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPT 118
Db   90 PDYKDR--LSLSENYTLSIKNARISDEKRFVCMLVT-EDDVSEEPTVVKV------FKQ 139

Qy   119 PS------ISDFEIPTSNIRRI-ICSTSGGFPEPHLSWLENG------EELNAINTTVSQ 165
Db   140 PSQPELLHQADF-LETEKLRKMLGECVVRDSTPEGNVTWYKNGRVLQPVEEVVVINLRKVE 198

Qy   166 DPEFEELYAVSSKLDFNMT----TNHSFMCLLIKY 194
Db   199 NRSTGLFTMTSSLQYMPTKEDANAKFTCIVTY 230

RESULT 14
BUTY_MOUSE

ID   BUTY_MOUSE   STANDARD;   PRT;   524 AA.
AC   Q62556; P97392;
DT   01-NOV-1997 (Rel. 35, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Butyrophilin precursor (BT).
GN   BTN1A1 OR BTN.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129; TISSUE=Mammary gland;
RX   MEDLINE=97148936; PubMed=995761;
RA   Ogg S.L., Komaragiri M.V.S., Mather I.H.;
RT   "Structural organization and mammary-specific expression of the
RT   butyrophilin gene.";
RL   Mamm. Genome 7:900-905(1996).
RN   [2]
RP   SEQUENCE OF 39-487 FROM N.A.
RC   TISSUE=Mammary gland;
RX   MEDLINE=96125722; PubMed=8541302;
RA   Ishii T., Aoki N., Noda A., Adachi T., Nakamura R., Matsuda T.;
RT   "Carboxy-terminal cytoplasmic domain of mouse butyrophilin
RT   specifically associates with a 150-kDa protein of mammary epithelial
RT   cells and milk fat globule membrane.";
RL   Biochim. Biophys. Acta 1245:285-292(1995).
CC   -!- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
CC   MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
CC   ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
CC   MEMBRANE (BY SIMILARITY).
CC   -!- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN
CC   ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSION INCREASES DURING THE LAST HALF OF
CC   PREGNANCY AND IS MAXIMAL DURING LACTATION.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC   SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC   ---

DR   EMBL; U67065; AAB51034.1; -.
DR   EMBL; S80642; AAB35893.1; -.
DR   MGD; MGI:103118; Btnla1.
DR   InterPro; IPR001870; Gamma_carbxylse.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   InterPro; IPR003877; SPRY.
DR   InterPro; IPR003878; SPRY_domain.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00622; SPRY; 1.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00449; SPRY; 1.
KW   Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL   1   26
FT   CHAIN   27   524
FT   DOMAIN   27   247   BUTYROPHILIN.
FT   TRANSMEM   248   268   POTENTIAL.
FT   DOMAIN   269   524   EXTRACELLULAR (POTENTIAL).
FT   DOMAIN   CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD   56   56   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   216   216   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT   46   46   D -> DD (IN REF. 2).
FT   CONFLICT   117   117   V -> F (IN REF. 2).
FT   CONFLICT   191   191   E -> V (IN REF. 2).
FT   CONFLICT   210   210   R -> S (IN REF. 2).
FT   CONFLICT   363   363   V -> E (IN REF. 2).
FT   CONFLICT   408   408   T -> K (IN REF. 2).
FT   CONFLICT   413   414   SL -> FF (IN REF. 2).
FT   CONFLICT   420   423   PRRV -> LAEY (IN REF. 2).
FT   CONFLICT   492   509   DIPLSPLGEGCTSGDKDT -> GHSLVPAGGRLYFWRQRH
FT   (IN REF. 2).
SQ   SEQUENCE   524 AA; 58406 MW; 333F4DE2C7704480 CRC64;

Query Match   10.4%; Score 119; DB 1; Length 524;
Best Local Similarity   23.8%; Pred. No. 0.011;
Matches   44; Conservative 34; Mismatches 87; Indels 20; Gaps 7;

Qy   20 ATLSCGH--NVSEELAQTRIYWQKEKKMVLTMMSGD-----MNIWPEYKNR---TIFD 68
            |:|:|| || ::| | | |:| | ::| | | :||
Db   47 AELTCGFSPNASSEYM---ELLWFRQTRSTAVLLYRDGQEQGQOMTEYRGRATLATAGL 103

Qy   69 ITNNLSIVILALRPSDEGSTYECVVLKEKDAFKREHLAEVTLSVKADFPTPSISDFEIPT 128
            :|| ||||| :||| | || | | | | || ||| | | | | |
Db 104 LDGRATLLIRDVRVSDQGEYRC--LFKDNDDEE---AAVYLKVAAVGSDPQIS-MTVQE 157

Qy 129 SNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSF 188
            :::|| || ||| | ||| | | | | | | | : | | || ||
Db 158 NGEMELECTSGWYPEPQVQWRGNREMLPSTSESKHNEEGLFTVAVSMMIRDSSIKNM 217

Qy 189 MCLIK 193
            |:||
Db 218 SCCIQ 222

RESULT 15

ID   NCA1_XENLA   STANDARD;   PRT;   1088 AA.
AC   P16170;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Neural cell adhesion molecule 1, large isoform precursor (N-CAM 180)
DE   (Contains: N-CAM 140).
GN   NCAM1.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90098871; PubMed=2481269;
RA   Krieg P.A., Sakaguchi D.S., Kintner C.R.;
RT   "Primary structure and developmental expression of a large
RT   cytoplasmic domain form of Xenopus laevis neural cell adhesion
RT   molecule (NCAM).";
RL   Nucleic Acids Res. 17:10321-10335(1989).
CC   -!- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
CC   NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
CC   NEURITES, ETC.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS OF
CC   N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN NEURON AND IN PRESUMPTIVE NEURAL
CC   TISSUE.
CC   -!- DEVELOPMENTAL STAGE: THE MRNA ENCODING THIS LD-NCAM IS THE MAJOR
CC   TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING
CC   EARLY NEURAL DEVELOPMENT.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC   --
DR   EMBL; M25696; AAA49909.1; -.
DR   PIR; S09600; LJXLNL.
DR   HSSP; P56276; 1TLK.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IG2; 5.
KW   Neural cell adhesion; Glycoprotein; Transmembrane; Repeat; Brain;
KW   Immunoglobulin domain; Alternative splicing; Signal.
FT   SIGNAL   1   19
FT   CHAIN   20   1088   NEURAL CELL ADHESION MOLECULE 1, LARGE
FT   ISOFORM.
FT   DOMAIN   20   705   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   706   723   POTENTIAL.
FT   DOMAIN   724   1088   CYTOPLASMIC (POTENTIAL).
FT   DOMAIN   34   100   IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN   129   193   IG-LIKE C2-TYPE DOMAIN 2.
FT   DOMAIN   225   289   IG-LIKE C2-TYPE DOMAIN 3.
FT   DOMAIN   316   386   IG-LIKE C2-TYPE DOMAIN 4.
FT   DOMAIN   413   480   IG-LIKE C2-TYPE DOMAIN 5.
FT   DOMAIN   512   589   FIBRONECTIN TYPE-III 1.
FT   DOMAIN   618   686   FIBRONECTIN TYPE-III 2.
FT   DOMAIN   149   153   HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN   158   162   HEPARIN-BINDING (POTENTIAL).
FT   DISULFID   41   93   PROBABLE.
FT   DISULFID   136   186   PROBABLE.
FT   DISULFID   232   282   PROBABLE.
FT   DISULFID   323   379   PROBABLE.
FT   DISULFID   420   473   PROBABLE.
FT   CARBOHYD   82   82   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   219   219   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   310   310   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   341   341   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   417   417   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   443   443   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   472   472   N-LINKED (GLCNAC...) (POTENTIAL).

```
FT   VARSPLIC    804   1049         MISSING (IN ISOFORM N-CAM 140).
SQ   SEQUENCE  1088 AA;  117778 MW;  62738B55B03F3E83 CRC64;

Query Match          10.1%;  Score 116.5;  DB 1;  Length 1088;
Best Local Similarity  24.0%;  Pred. No. 0.044;
Matches   43;  Conservative  31;  Mismatches  58;  Indels  47;  Gaps  9;

Qy     18 EVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRTIFDITNNLSIVI 77
             | | :| : | | | | : | | :| | :| : | | : | : | | :|
Db    130 EDAVIICDVSSSIPSI----ITWRHKGKDVI----------------FKKDVRFVVLANNVLQI 173

Qy     78 LALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPTPSISDFEI---PTSNIRR- 133
            :: :|||||| |            | |: ::  |:|      | |:|
Db    174 RGIKKTDEGTYRC----EGRILARGEINYKDIQVIVNVP-PTIQARQLRVNATANMAES 227

Qy    134 -IICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN----MTTNH 186
            :: |||:|:|||:|:|| :  |                        |:|  : |
Db    228 VVLSCDADGFPDPEISWLKKGEPI---------EDGE-------EKISFNEDQSEMTIHH 271
```

Search completed: `October 17, 2002, 16:36:54
Job time : 15 secs

OM protein - protein search, using sw model

```
                    GenCore version 5.1.3
          Copyright (c) 1993 - 2002 Compugen Ltd.
```

Run on: October 17, 2002, 16:35:40 ; Search time 27 Seconds
                 (without alignments)
                 1383.959 Million cell updates/sec

Title: US-09-454-651B-23
Perfect score: 1149
Sequence: 1 GLSHFCSGVIHVTKEVKEVA.........LRVNQTFNWNTKQEHFPDN 216

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :   SPTREMBL_19:*
                 1: sp_archea:*
                 2: sp_bacteria:*
                 3: sp_fungi:*
                 4: sp_human:*
                 5: sp_invertebrate:*
                 6: sp_mammal:*
                 7: sp_mhc:*
                 8: sp_organelle:*
                 9: sp_phage:*
                 10: sp_plant:*
                 11: sp_rodent:*
                 12: sp_virus:*
                 13: sp_vertebrate:*
                 14: sp_unclassified:*
                 15: sp_rvirus:*
                 16: sp_bacteriap:*
                 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1118	97.3	288	6	O77684	macaca neme
2	1100	95.7	288	6	Q28499	macaca mula
3	1085	94.4	288	6	Q9BDN6	cercocebus
4	1085	94.4	289	6	Q28347	cercocebus
5	764	66.5	230	6	Q9N2I3	sus scrofa
6	762.5	66.4	288	6	Q9TT70	sus scrofa
7	762.5	66.4	297	6	Q9BE99	sus scrofa
8	761	66.2	229	6	Q9TT71	sus scrofa
9	761	66.2	292	6	Q9GMZ8	sus scrofa
10	743	64.7	292	6	O02758	felis silve
11	743	64.7	304	6	Q9TQX1	felis famil
12	719	62.6	296	6	O46405	felis famil
13	717.5	62.4	235	6	O46405	bos taurus
14	705	61.4	235	6	Q9TGS8	canis famil
15	603.5	52.5	321	11	O35187	canis famil
16	602	52.4	290	11	Q62680	rattus norv
17	601.5	52.3	321	11	Q62624	rattus norv
18	596	51.9	321	11	O55202	rattus norv
19	560	48.7	306	11	Q9R129	mus musculu
20	350	30.5	174	6	Q9GMZ9	felis silve
21	349.5	30.4	173	6	Q95L17	felis silve
22	255.5	22.2	212	11	Q61332	mus musculu
23	255.5	22.2	329	6	Q9XSX6	felis silve
24	200.5	17.4	332	6	Q9GMZ7	felis silve
25	200.5	17.4	332	6	Q95L16	felis silve
26	188.5	16.4	280	6	Q9TTF1	canis famil
27	188.5	16.4	296	13	O42404	gallus gall
28	182	15.8	329	6	Q9TTF2	canis famil
29	178	15.5	323	6	Q9BDM2	cercopithec
30	177	15.4	323	6	Q9BDM9	macaca neme
31	177	15.4	323	6	Q9BDM4	macaca mula
32	176	15.3	275	6	Q9BDN9	papio anubi
33	176	15.3	323	6	Q9BDB8	cercocebus
34	171	14.9	284	6	Q9GL33	cercocebus
35	162	14.1	313	11	O35531	rattus norv
36	161.5	14.1	325	6	O02838	sus scrofa
37	156.5	13.6	290	4	Q9NZQ7	homo sapien
38	153	13.3	290	11	Q9EP73	mus musculu
39	153	13.3	356	11	Q64381	mus musculu
40	153	13.2	314	11	Q61238	mus musculu
41	150	13.1	309	11	Q91YV7	mus musculu
42	142	12.4	316	4	Q9BXR1	homo sapien
43	139.5	12.1	521	6	O46651	oryctolagus
44	138	12.0	509	11	P97710	rattus norv
45	137	11.9	509	11	Q9QWI5	rattus norv

ALIGNMENTS

RESULT 1
O77684

```
ID   O77684       PRELIMINARY;      PRT;   288 AA.
AC   O77684;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PROTEIN.
B7.
GN   B7.
OS   Macaca nemestrina (Pig-tailed macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9545;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kraus G., Hnatyszyn J.H.;
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
     EMBL; AF079519; AAC31555.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_like.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
SQ   SEQUENCE 288 AA;  33131 MW;  76BBC42839E9AB79 CRC64;
```

Query Match   97.38; Score 1118; DB 6; Length 288;
Best Local Similarity   97.7%;
Matches 210; Conservative   1; Mismatches   4; Indels   0; Gaps   0;

```
Qy    2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 61
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 87

Qy   62 KNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPPSI 121
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   88 KNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVMLSVKADFPTPSI 147
```

```
Qy  122 SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
        ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db  148 TDFEIPPSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYTVSSKLDFN 207

Qy  182 MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
        |||||||||||||||||||||||||||||| ||||
Db  208 MTTNHSFMCLIKYGHLRVNQTFNWNTTPKQEHFPDN 242
```

RESULT 2

```
ID   Q28499                  PRELIMINARY;     PRT;   288 AA.
AC   Q28499;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   B7 PROTEIN (CD80 PROTEIN PRECURSOR).
GN   B7 OR N939.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BLOOD;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing and homology analysis of nonhuman primate
RT   Fas/Fas-Ligand and co-stimulatory molecules.";
RL   Immunogenetics 0:0-0(2001).
DR   EMBL; U19840; AAA86706.1; -.
DR   EMBL; AF344849; AAK37609.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
KW   Signal.
FT   SIGNAL          1     26       POTENTIAL.
SQ   SEQUENCE   288 AA;  33141 MW;  E70BEA4006C7A609 CRC64;

Query Match          95.7%;  Score 1100;  DB 6;  Length 288;
Best Local Similarity 96.3%;  Pred. No. 2.2e-94;
Matches 207;  Conservative 2;  Mismatches 6;  Indels 0;  Gaps 0;

Qy    2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMYLTMMSGDMNIWPEY 61
        |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   28 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 87

Qy   62 KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPSI 121
        |||  ||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   88 KNRIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADPPTPSI 147

Qy  122 SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
        |||||| |||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db  148 TDFEIPPSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYTVSSKLDFN 207

Qy  182 MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
        |||||||||||||||||||||||||||||| ||||
Db  208 MTTNHSFMCLIKYGHLRVNQTFNWNTTPKQEHFPDN 242
```

RESULT 3

```
ID   Q9BDN6                  PRELIMINARY;     PRT;   288 AA.
AC   Q9BDN6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CD80 PROTEIN.
GN   MNB71.
OS   Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercocebus.
OX   NCBI_TaxID=9531;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BLOOD;
RX   MEDLINE=21383618; PubMed=11491535;
RA   Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 53:315-328(2001).
DR   EMBL; AF344839; AAK37535.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
SQ   SEQUENCE   288 AA;  32917 MW;  C6A3F6A3C592972B CRC64;

Query Match          94.4%;  Score 1085;  DB 6;  Length 288;
Best Local Similarity 95.3%;  Pred. No. 5.4e-93;
Matches 205;  Conservative 4;  Mismatches 6;  Indels 0;  Gaps 0;

Qy    2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMYLTMMSGDMNIWPEY 61
        ||||||||||||||||||||||||||||||||||||:  |||||||:||||||||||||
Db   28 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQCKEKKMVLMISGDMNIWPEY 87

Qy   62 KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPSI 121
        |||  ||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   88 KNRIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADPPTPSI 147

Qy  122 SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
        |||||| ||||||||||||||||||||||||||||||| ||||||||||| |||||||||
Db  148 TDFEIPPSNIRRIICSTSGGFPEPHLSWLENGEELNAIDTTVSQDPETELYTVSSKLDFN 207

Qy  182 MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
        |||||||:|||||||||||||||||||||| ||||
Db  208 MTTNHSFVCLIKYGHLRVNQTFNWNTTPKQEHFPDN 242
```

RESULT 4

```
ID   Q28347                  PRELIMINARY;     PRT;   289 AA.
AC   Q28347;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   B7 PROTEIN (FRAGMENT).
GN   B7.
OS   Cercocebus torquatus (red-crowned mangabey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercocebus.
OX   NCBI_TaxID=9530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BLOOD;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
DR   EMBL; U19833; AAA86700.1; -.

Query Match          94.8%;  Score 1085;  DB 6;  Length 288;
Best Local Similarity 95.3%;  Pred. No. 5.4e-93;
Matches 205;  Conservative 4;  Mismatches 6;  Indels 0;  Gaps 0;

Qy    2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMYLTMMSGDMNIWPEY 61
        ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   28 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 87

Qy   62 KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPSI 121
        |||  ||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   88 KNRIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADPPTPSI 147

Qy  122 SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
        |||||| |||||||||| ||||||||||||||||||| |||||||||||| |||||||||
Db  148 TDSEIPPSNIRRIICSNSGGFPEPHLSWLENGEELNAISTTVSQDPETELYTVSSKLDFN 207

Qy  182 MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
        |||||||:|||||||||||||||||||||| ||||
Db  208 MTTNHSFVCLIKYGHLRVNQTFNWNTTPKQEHFPDN 242
```

```
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00410; IG_like; 2.
FT   NON_TER      289    289
SQ   SEQUENCE   289 AA;  33030 MW;  5ED6A3F6A3C59297 CRC64;

Qy     2  LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY   61
          |||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||||
Db    28  LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYCQKEKKMVLTMISGDMNIWPEY   87

Qy    62  KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI  121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    88  KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI  147

Qy   122  SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDEN  181
          :||||| |||||||||||||||||||||||||| |||||:||||||||||||:|||||||
Db   148  TDFEIPPSNIRRIICSTSGGFPEPHLSWLENGGELNAIDTTVSQDPETELYTVSSKLDFN  207

Qy   182  MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN  216
          |||||||:||||||||||||||||||| ||||||||
Db   208  MTTNHSFVCLIKYGHLRVNQTFNWNTPKQEHFPDN  242


RESULT 5
ID   Q9N2I3
AC   Q9N2I3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CD80 PROTEIN PRECURSOR.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LANDRACE; TISSUE=SPLEEN;
RA   Wada M., Amae S., Hoshi M., Nio M., Ohi R.;
RL   "Porcine CD80(B-7) mRNA, partial cds.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB026121; BAA90700.2; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
KW   CD80/B7.
FT   SIGNAL.            1      29    POTENTIAL.
FT   CHAIN             30     230
SQ   SEQUENCE   230 AA;  26028 MW;  EB63AD172663C4A4 CRC64;

Query Match   67.0%;  Score 764;  DB 6;  Pred. No. 3e-63;  Length 230;
Best Local Similarity   66.5%;
Matches  140;  Conservative  26;  Mismatches  43;  Indels  0;  Gaps  0;

Qy     1  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE   60
          ||:|||||:|:||:||||:|||||:|:||||||||:||||||:|||||||| |||:|||:|
Db    22  GLFDFCSGIVQVTKTVKEIAVLSCDYNISTEELTRVRIYWQKDNEMVLAVMSGKVKVWPK   81

Qy    61  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS  120
          |:|||||| |||||||||||| ||:|||:||| |||  ||||||||:||| |||||:|
Db    82  YENRTFDVTNNLCIVILALRLSDNGTYTCVVQKERGSYKLEHLTSVKLMVKADPPVPS  141

Qy   121  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF  180
          |:|||||||||||||||||||||||||||||||| ||||:||||||||||||:||||||:
Db   142  ITALGNPSPNIKRIRCSTSGGFPEPHLSWLENGEELNATNTMLSQDPETELYMISSELDF  201

Qy   181  NMTTNHSFMCLIKYGHLRVNQTFNW-NTTKQE  211
          | ||||||||||:|||| |:|||||| |:||:|
Db   202  NVTGNHSFMCLIVKYGGLTVSQFNWQKSAKRE  233
```

```
Db   142  ITALGNPSPNIKRIRCSTSGGFPEPHLSWLENGEELNATNTMLSQDPETELYMISSELDF  201

Qy   181  NMTTNHSFMCLIKYGHLRVNQTFNWNTTK  209
          | ||||||||||:|||| |:|||||:|:|||
Db   202  NVTGNHSFMCLIVKYGGLTVSQQTFNWQKCK  230


RESULT 6
ID   Q9TT70
AC   Q9TT70;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CD80 PROTEIN PRECURSOR (FRAGMENT).
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
SEQUENCE FROM N.A.
EMBL; AF203443; AAF22750.1; -.
J. Immunol. 164:6340-6348(2000).
RT   Alternatively Spliced Form of B7-1.";
"Primary Structure and Functional Characterization of a Soluble,
RA   Fodor W.L., Mueller J.P., Matis L.A., Rother R.P.;
RA   Faas S.J., Giannoni M.A., Mickle A., Kiesecker C.L., Reed D.J., Wu D.,
RX   MEDLINE=20302785; PubMed=10843688;
RP   SEQUENCE FROM N.A.
SQ   SEQUENCE   288 AA;  32510 MW;  CD80 PROTEIN.
NON_TER      1      29
SIGNAL.
SMART; SM00410; IG; 1.
SMART; SM00409; IG; 2.
Pfam; PF00047; ig; 2.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003600; Ig_like.
InterPro; IPR003599; Ig.
CHAIN       30     >288

Query Match   66.4%;  Score 762.5;  DB 6;  Pred. No. 5.6e-63;  Length 288;
Best Local Similarity   66.5%;
Matches  141;  Conservative  28;  Mismatches  42;  Indels  1;  Gaps  1;

Qy     1  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE   60
          ||:|||||:|:||:||||:|||||:|:||||||||:||||||:|||||||| |||:|||:|
Db    22  GLFDFCSGIVQVTKTVKEIAVLSCDYNISTEELTRVRIYWQKDNEMVLAVMSGKVKVWPK   81

Qy    61  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS  120
          |:|||||| |||||||||||| ||:|||:||| |||  ||||||||:||| |||||:|
Db    82  YENRTFDVTNNLCIVILALRLSDNGTYTCVVQKERGSYKLEHLTSVKLMVKADPPVPS  141

Qy   121  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF  180
          |:|||||||||||||||||||||||||||||||| ||||:||||||||||||:||||||:
Db   142  ITALGNPSPNIKRIRCSTSGGFPEPHLSWLENGEELNATNTMLSQDPETELYMISSELDF  201

Qy   181  NMTTNHSFMCLIKYGHLRVNQTFNW-NTTKQE  211
          | ||||||||||:|||| |:|||||| |:|:|
Db   202  NVTGNHSFMCLIVKYGGLTVSQQTFNWQKSAKRE  233


RESULT 7
ID   Q9BE99
AC   Q9BE99;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CD80 PROTEIN PRECURSOR.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
SQ   SEQUENCE   297 AA;
```

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LANDRACE; TISSUE=ILEUM MUCOSA;
RA Wada M., Amae S., Sano N., Ishii T., Hoshi M., Nio M.,
RA Hayashi Y., Ohi R.;
RT "Cloning and sequencing of cDNAs for porcine B7-1 (CD80) and soluble
RT isoforms.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB049760; BAB40952.1; -.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR SMART; SM00410; IG_like; 1.
KW Signal.
FT SIGNAL 1 29
FT CHAIN 30 297
SQ SEQUENCE 297 AA; 33438 MW; 2310971IEA63EF23 CRC64;

Query Match 66.4%; Score 762.5; DB 6; Length 297;
Best Local Similarity 66.5%; Pred. No. 5.8e-63;
Matches 141; Conservative 28; Mismatches 42; Indels 1; Gaps 1;

POTENTIAL.
CD80 PROTEIN.

Qy 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 22 GLFDFCSGIVQVTKTVKEIAVLSCDYNISTEELITRVRIYWQKDNEMVLAVMSGKVKVWPK 81

Qy 61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 82 YENRTFTDVTNNLCIVILALRLSDNGTYTCVVQKRERGSYKLEHLTSVKLMVKADFPVPS 141

Qy 121 ISDFEIPTSNIRRICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 142 ITALGNPSPNIKRIRCSTSGGFPEPHLSWLENGEELNATNTMLSQDPETELYMISSELDF 201

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNW-NTTKQE 211
       ||||||||||||||||||||||||| ||| :|
Db 202 NVTGNHSFMCLVKYGGLTVSQTFNW QKSAKRE 233

RESULT 8
Q9TT71
ID Q9TT71 PRELIMINARY; PRT; 229 AA.
AC Q9TT71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CD80 PROTEIN PRECURSOR.
GN CD80 OR CD80/B7-1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Faas S.J., Giannoni M.A., Mickle A., Kiesecker C.L., Reed D.J., Wu D.,
RA Fodor W.L., Meuller J.P., Matis L.A., Rother R.P.;
RT "Primary Structure and Functional Characterization of a Soluble,
RT Alternatively Spliced Form of B7-1.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Wada M., Amae S., Hoshi M., Nio M., Ishii T., Sano N., Sasaki H.,
RA Ohi R.;
RT "Splicing Isoform of Porcine CD80.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF203442; AAF22749.1; -.
DR EMBL; AB038153; BAA90764.1; -.
DR InterPro; IPR003599; Ig.

RESULT 9
Q9GMZ8
ID Q9GMZ8 PRELIMINARY; PRT; 292 AA.
AC Q9GMZ8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE B-LYMPHOCYTE ACTIVATION ANTIGEN B7-1 (CD80).
RX MEDLINE=20485322; PubMed=11029611;
RA Nishimura Y., Shimojima M., Miyazawa T., Sato E., Nakamura K.,
RA Izuniya Y., Ikeda Y., Mikami T., Takahashi E.;
RT "Molecular cloning of the cDNA encoding the feline B-lymphocyte
RT activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which
RT interact with human CTLA4-Ig.";
RL Eur. J. Immunogenet. 27:427-430(2000).
DR EMBL; AB030651; BAB11687.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG_like; 2.
SQ SEQUENCE 292 AA; 33540 MW; ED9AECE10D30401 CRC64;

CD80.
Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
NCBI_TaxID=9685;

Query Match 66.2%; Score 761; DB 6; Length 229;
Best Local Similarity 67.8%; Pred. No. 5.7e-63;
Matches 139; Conservative 26; Mismatches 40; Indels 0; Gaps 0;

CD80 PROTEIN.
C3ADI72663C4A4ED CRC64;

Qy 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
      |||:||||:| | ||||:|| ||:|||:.||:|:|:.||||||:|:||| :||:|.:.||
Db 22 GLFDFCSGIVQVTKTVKEIAVLSCDYNISTEELITRVRIYWQKDNEMVLAVMSGKVKVWPK 81

Qy 61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
      |:|||.| |.|||.|||||||.||:|||.|||:|.:: ||.||:|||.||||::||||.||
Db 82 YENRTFTDVTNNLCIVILALRLSDNGTYTCVVQKRERGSYKLEHLTSVKLMVKADFPVPS 141

Qy 121 ISDFEIPTSNIRRICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
       |:|. :||||:|||||||||||||||||||||||||.||.:.|||||||||.:||.||
Db 142 ITALGNPSPNIKRIRCSTSGGFPEPHLSWLENGEELNATNTMLSQDPETELYMISSELDF 201

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNW 205
       |:|.|||||||:|||.| ||||||||
Db 202 NVTGNHSFMCLVKYGGLTVSQTFNW 226

RESULT 10 (lower right)
Q9GMZ8
ID Q9GMZ8 PRELIMINARY; PRT; 292 AA.
AC Q9GMZ8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE B-LYMPHOCYTE ACTIVATION ANTIGEN B7-1 (CD80).
RX MEDLINE=20485322; PubMed=11029611;
RA Nishimura Y., Shimojima M., Miyazawa T., Sato E., Nakamura K.,
RA Izuniya Y., Ikeda Y., Mikami T., Takahashi E.;
RT "Molecular cloning of the cDNA encoding the feline B-lymphocyte
RT activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which
RT interact with human CTLA4-Ig.";
RL Eur. J. Immunogenet. 27:427-430(2000).
DR EMBL; AB030651; BAB11687.1; -.
CD80.
Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
NCBI_TaxID=9685;

Query Match 64.7%; Score 743; DB 6; Length 292;
Best Local Similarity 63.3%; Pred. No. 3.7e-61;
Matches 136; Conservative 33; Mismatches 44; Indels 2; Gaps 1;

Qy 2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 61
      :||||||:|:||||||:||:||||:|:|:.||:|:|::.||||||:|:||| :||:|::||
Db 28 LFYFCSGIIQVNKTVEEVAVLSCDYNISTEELTEIRIYWQKDDEMVLAVMSGKVQVWPKY 87

Qy 62 KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
      :|||.| |.|||.||||||.||:|||.|||:|.:: :||.||:|||.||||::||||.||
Db 88 KNRTFDVTDNISIVIMALRLSDNGKYTCICIQKIEKGSYKVKHLTSVMLLVRADFPVPSI 147

RESULT 10

```
Qy  122 SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
        :|:|:|:| || |||||:| |||||:|| :||||:|||||||||||||||||||:|:||||
Db  148 TDLGNPSHNIKRIMCLTSGGFPKPHLSWLENEEELNAINTTVSQDPETELYTISSELDFN 207

Qy  182 MTTNHSFEMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
        |||||||:|:|||:|||||:|:||||||||
Db  208 MTNNHSFCLIVKYGNLLVSQIFNWQ--KSEPQPSN 240
```

```
ID   002758      PRELIMINARY;      PRT;   292 AA.
AC   002758;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   T-CELL SPECIFIC SURFACE GLYCOPROTEIN B7-1.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hash S.M., Collison E.W.;
RT   "Felis catus t-cell specific surface glycoprotein B7-1.";
RL   Thesis (1996), Veterinary Pathobiology, Texas A&M Univ.
DR   EMBL; U57755; AAB53575.1; -.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00410; IG_like; 2.
SQ   SEQUENCE   292 AA;   33482 MW;  6F117E7852B7950F CRC64;
```

```
Query Match             64.78%;  Score 743;  DB 6;  Length 292;
Best Local Similarity   63.3%;   Pred. No. 3.7e-61;
Matches  136;  Conservative  33;  Mismatches  44;  Indels  2;  Gaps  1;

Qy   2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 61
        :||||:| |||||||||||||| |:|:|  :||||:|||||  ||:||:||:| :|:
Db  28 LFYFCSGIIQVNKTVKEVAVLSCDYINISTKELIEIRIYWQKDDEMVLAVMSGKVQVWPKY 87

Qy  62 KNRTFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
        ||||||  : |:||:||||:||:|:|:| :|:|:|:  ||:| |:|||:||:|||||||
Db  88 KNRTFDTVDTNHSIVIMALRLSDNGKYTCIIQKIEKGSYKVKHLTSVMLLVRADFPVPSI 147

Qy 122 SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
Db 148 TDLGNPSHNIKRIMCLTSGGFPKPHLSWLENEEELNAINTTVSQDPETELYTISSELDFN 207

Qy 182 MTTNHSFEMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
Db 208 MTNNHSFCLIVKYGNLLVSQIFNWQ--KSEPQPSN 240
```

RESULT 11

```
ID   Q9TQX1      PRELIMINARY;      PRT;   304 AA.
AC   Q9TQX1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   B7-1 PROTEIN PRECURSOR.
GN   CD80.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20093996; PubMed=10630300;
RA   Yang S., Sim G.-K.;
RT   "New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
RT   Molecules.";
RL   Immunogenetics 50:349-353(1999).
DR   EMBL; AF106824; AAF17295.1; -.
DR   EMBL; AF106833; AAF17293.1; -.
DR   EMBL; AF106829; AAF17293.1; JOINED.
DR   EMBL; AF106830; AAF17293.1; JOINED.
DR   EMBL; AF106831; AAF17293.1; JOINED.
DR   EMBL; AF106832; AAF17293.1; JOINED.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
KW   Signal.
FT   SIGNAL        1     33
FT   CHAIN        34    304       B7-1 PROTEIN.
SQ   SEQUENCE   304 AA;   34454 MW;  09E082F6BB06C94F CRC64;
```

```
Query Match             62.68%;  Score 719;  DB 6;  Length 304;
Best Local Similarity   60.5%;   Pred. No. 6.7e-59;
Matches  130;  Conservative  36;  Mismatches  49;  Indels  0;  Gaps  0;

Qy   2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 61
Db  28 LFYFCSGIIQVNKTVKEVAVLSCDYINISTELMKVRIYWQKDDEVVLAVISGQTKWWSKY 87

Qy  62 KNRTFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
Db  88 ENRTFADFTNNLSIVIMALRLSDNGKYTCIVQKTEKRSYKVKHMTSVMLLVRADFPVPSI 147

Qy 122 SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
Db 148 TDLGNPSHDIKRIMCLTSGGFPKPHLSWWENEEELNAANTTVSQDDPETELYTISSELDFN 207

Qy 182 MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
Db 208 ITSNHSFVCLVKYGDLTVSQIFNWQKSVEPHPPNN 242
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RESULT 12

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ID   O46405      PRELIMINARY;      PRT;   296 AA.
AC   O46405;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CD80 ANITGEN PRECURSOR (FRAGMENT).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99115507; PubMed=9914337;
RA   Parsons K.R., Howard C.;
RT   "Cloning of cattle CD80.";
RL   Immunogenetics 49:231-234(1999).
DR   EMBL; Y09950; CAA71081.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
KW   Signal.
FT   SIGNAL        1     25
FT   NON_TER       1
FT   NON_TER     296
SQ   SEQUENCE   296 AA;   33618 MW;  7ADB11FB5F532EF5 CRC64;
```

```
Query Match             62.48%;  Score 717.5;  DB 6;  Length 296;
Best Local Similarity   63.2%;   Pred. No. 9e-59;
```

Matches 134; Conservative 28; Mismatches 47; Indels 3; Gaps 2;

```
Qy      1 GLSHFCSGVI--HVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIW 58
          || :||||||   ||| ||| ||| :|||| ||||||||||||||||||||||||||
Db     27 GLFYFCSGITPKSVTKRVEAVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILPGSKVQVW 86

Qy     59 PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYE-KDAFKREHLAEVTLSVKADFP 117
          |||||||||| || || |||||||||||||||| | :||||||| ||||||||||||
Db     87 PEYKNRRTITDMDNPRIVILALRLSDSGTYTCVIQKPDLKGAYKLEHLTSVRLMIRADPP 146

Qy    118 TPSISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSK 177
          :|:| |  ||||||||||||||||||||||||||||||||||| ||||| :||:
Db    147 VPINDLGNPSPNIRRLICSTSGGFPRHLYKLENGEELNATNTTLSQDPETKLYIMISSE 206

Qy    178 LDENMTTNHSFMCLIKYGHLRVNQTFNNNTTK 209
          |||||||||||||||||||||||| :| :|
Db    207 LDFNMISNHSFCLVKYGDLTVSQIFNWQESK 238
```

```
Qy      2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 61
          |||||||||||| ||| ||||||||||||||||||||||||||||||||||||||||:|
Db     28 LFYFCSGIIQVNKTVKEVAVLSCDYNISTTELMKVRIYWQKDDEVVLAVTSGQTKVWSKY 87

Qy     62 KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db     88 ENRTPADFTNNLSIVIMALRLSDNGKYTCIVQKTEKRSYXVKHMISVMLLVRADPPVPSI 147

Qy    122 SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
          :| :|||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db    148 TDLGNPSHDIKRIMCSTSGGFPKHLSWWENEEELNAANTTVSQDPDTELYTISSELDFN 207

Qy    182 MTTNHSFMCLIKYGHLRVNQTFNNNTTK 209
          :|:|||:|||||||||||| ||| ||| 
Db    208 ITSNHSFVCLVKYGDLTVSQIFNWQCCK 235
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Query Match   61.4%; Score 705; DB 6; Length 235;
Best Local Similarity 61.5%; Pred. No. 9.7e-58;
Matches 128; Conservative 33; Mismatches 47; Indels 0; Gaps 0;

```
Qy      2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 61
          |||||||||||| ||| ||||||||||||||||||||||||||||||||||||||||:|
Db     28 LFYFCSGIIQVNKTVKEVAVLSCDYNISTTELMKVRIYWQKDDEVVLAVTSGQTKVWSKY 87

Qy     62 KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db     88 ENRTPADFTNNLSIVIMALRLSDNGKYTCIVQKTEKRSYXVKHMISVMLLVRADPPVPSI 147

Qy    122 SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
          :| :|||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db    148 TDLGNPSHDIKRIMCSTSGGFPKHLSWWENEEELNAANTTVSQDPDTELYTISSELDFN 207

Qy    182 MTTNHSFMCLIKYGHLRVNQTFNNNTTK 209
          :|:|||:|||||||||||| ||| ||| 
Db    208 ITSNHSFVCLVKYGDLTVSQIFNWQCCK 235
```

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DR   EMBL; AF010465; AAB66351.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
SQ   SEQUENCE   321 AA;  36351 MW;  071C6007FBBD1E60 CRC64;

Query Match             52.5%;  Score 603.5;  DB 11;  Length 321;
Best Local Similarity   54.9%;  Pred. No. 4.1e-48;
Matches  113;  Conservative  34;  Mismatches  58;  Indels   1;  Gaps   1;

Qy     1 GLSHFCSGVI-HVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKNVLTMMSGDMNIWP 59
         ||     |  | :| |  | :  ||    |     : | ||||| ::| || ::| : |
Db    31 GLFQISSGIVGQVSKSVREKALLSCDYKFCSEEQSIHRIYWQKHDKMVLSVISGVPEVWP 90

Qy    60 EYKNRFIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTP 119
         |||||  :|| |||| :  |   | :|||| ||| : :::    :|| |||||||||||
Db    91 EYKNRIVYDIANNYSFSLIGLILSDRGTYTCVVQRYEGESYVVKHLTTVELSVRADFPTP 150

Qy   120 SISDFELPTSNIRRICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 179
         :|::  | :|| ||:|| ||||| | |||||||| ||.|||| |||||:|||..||:|| |
Db   151 NITESGNPSADIKRITCFASGGFPKPRLSWLENGRELNGINTTISQDPESELYTISSQLD 210

Qy   180 FNMTTNHSFMCLIKYGHLRVNQTFNW 205
         || | :| : ||:: ||. |.||:.||
Db   211 FNTTYDHFIDCFIEYGDAHVSQNFTW 236

Search completed: October 17, 2002, 16:37:54
Job time : 29 secs
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                                                    GenCore version 5.1.3
                                    Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run On:          October 17, 2002, 16:35:35 ; Search time 31 Seconds
                                            (without alignments)
                                            773.934 Million cell updates/sec

Title:           US-09-454-651B-23
Perfect score:   1149
Sequence:        1 GLSHFCSGVIHVTKEVKEVA..........LRVNQTFNWNTTKQEHFPDN 216
Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5
Searched:        747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters:            747574
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_032802:*
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      2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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     22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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               %
Result       Query
No.   Score  Match  Length  DB ID        Description
----  -----  -----  ------  -----        -----------
  1   1149  100.0   288   16  AAR67989   Human B lymphocyte
  2   1149  100.0   288   18  AAW38414   B7-1. Homo sapien
  3   1149  100.0   288   20  AAW86004   Human B7 protein s
  4   1149  100.0   288   20  AAW67804   Human B7-2 antigen
  5   1149  100.0   288   21  AAW73640   Human B lymphocyte
  6   1149  100.0   288   21  AAB37087   Human B7 protein
  7   1149  100.0   288   21  AAY99966   Human B lymphocyte
  8   1149  100.0   288   21  AAY44289   Human B7.1 co-stim
  9   1149  100.0   288   22  AAY54920   Human B7.1 protein
 10   1149  100.0   288   22  AAU05121   Colorectal tumour
 11   1149  100.0   473   18  AAB19959   Human B lymphocyte
                          AAW41415   Human B7.1-murine
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ALIGNMENTS

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RESULT 1
AAR67989
ID   AAR67989 standard; Protein; 288 AA.
XX
AC   AAR67989;
XX
DT   21-AUG-1995  (first entry)
XX
DE   Human B lymphocyte antigen B7-1 (hB7-1).
XX
KW   B lymphocyte antigen; B7-1; B cell activation antigen; CD28;
KW   ligand; T cell surface antigen; transmembrane protein.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FH
FT   Protein        1..34
FT                  /label= signal sequence
FT   Domain         35..242
FT                  /note= "hydrophobic"
FT   Domain         243..269
FT                  /label= extracellular
FT   Domain         270..288
FT                  /label= transmembrane
FT   Misc-difference 53..55
FT                  /label= intracellular
FT   Misc-difference 89..91
FT                  /label= N-linked glycosylation
FT   Misc-difference 98..100
FT                  /label= see above
FT   Misc-difference 186..188
FT                  /label= see above
FT   Misc-difference 207..209
FT                  /label= see above
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 12  1146  99.7  251  20  AAW90208   hB7.1glu-glu solub
 13  1144  99.6  475  18  AAW38415   Soluble B7-1.lg.
 14  1143  99.5  488  20  AAW86004   Human B7-1.5T4.1 p
 15  1143  99.5  488  22  AAB33336   Amino acid sequenc
 16  1143  99.5  492  19  AAW42338   CD80-Ig-alpha-tp f
 17  1138  99.0  208  20  AAW90206   hB7.1Fc soluble fu
 18  1047  91.1  208  18  AAW35858   Human B7.1 for use
 19   761  66.2  229  22  AAY97780   Soluble porcine B7
 20   743  64.7  292  21  AAY32283   Feline CD80 (B7-1)
 21   743  64.7  292  21  AAY32276   Cat CD80 (B7-1)-TA
 22   739  64.3  292  21  AAY32284   Feline CD80 (B7-1)
 23   739  64.3  292  21  AAY32277   Cat CD80 (B7-1)-SY
 24   719  62.6  304  20  AAY41077   Canine B7-1 protei
 25   705  61.4  235  20  AAY41075   Canine B7-1S prote
 26   561  48.8  306  16  AAY82693   Mouse B7-1 alterna
 27   561  48.8  306  16  AAR67990   Murine B lymphocyt
 28   561  48.8  320  22  AAB19960   Mouse B lymphocyte
 29   561  48.8  306  16  AAR82692   Mouse B7-1 alterna
 30   558  48.6  306  20  AAW67805   Mouse B lymphocyte
 31   558  48.6  306  20  AAW73641   Mouse B7 antigen
 32   558  48.6  306  20  AAB37088   Mouse B lymphocyte
 33   558  48.6  306  21  AAY99967   Murine B7 protein
 34   349.5 30.4  173  20  AAY41082   Feline B7-1S prote
 35   311   27.1  214  16  AAR82901   Feline B7-1 (IgV-l
 36   305   26.5  200  16  AAR82900   Feline B7-1 (IgV-l
 37   250.5 21.8  212  16  AAR82902   Mouse B7-1 IgV-lik
 38   250.5 21.8  226  16  AAR82903   Mouse B7-1 IgV-lik
 39   200.5 17.4  329  21  AAY32285   Feline CD80 (B7-2)
 40   200.5 17.4  329  21  AAY32278   Cat CD80 (B7-2) li
 41   200.5 17.4  332  20  AAY41079   Feline B7-2 protei
 42   188.5 16.4  280  20  AAY41078   Canine B7-2S prote
 43   182   15.8  244  20  AAW90209   hB7.1his soluble f
 44   182   15.8  246  20  AAW86005   Human B7-2 extrace
 45   182   15.8  246  22  AAB83837   Amino acid sequenc
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FT   Misc-difference   211..213
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FT   Misc-difference   226..228
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FT   /label= Ig V-set domain
FT   Domain   139..236
FT   /label= Ig C-set domain
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PN   WO9503408-A.
XX
PD   02-FEB-1995.
XX
PF   26-JUL-1994;   94WO-US08423.
XX
PR   26-JUL-1993;   93US-0101624.
PR   19-AUG-1993;   93US-0109393.
PR   03-NOV-1993;   93US-0147773.
XX
PA   (DAND) DANA FARBER CANCER INST INC.
PA   (REPK) REPLIGEN CORP.
XX
PI   Freeman GJ, Gray GS, Greenfield E, Nadler LM;
XX
DR   WPI; 1995-075236/10.
DR   N-PSDB; AAQ081371.
XX
PT   Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful
PT   for enhancing or suppressing T-cell mediated immune responses
XX
PS   Disclosure; pages 111-113; 175pp; English.
XX
CC   Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,
CC   cell line Raji, clone no. 13. Its position in the genome is
CC   chromosome/segment 3. It was published by Freeman, F.J. et al.,
CC   J. of Immunology; 143: 8: 2714-2722, 15th October 1989. It can be
CC   found in Genbank at Accession no. M27533. The encoded protein,
CC   R67989, binds both human CTLA4 and human CD28. It is related
CC   to human hB7-2 (see Q81351) and murine hB7 (see Q81372).
XX
SQ   Sequence   288 AA;

Query Match   100.0%; Score 1149; DB 16; Length 288;
Best Local Similarity   100.0%; Pred. No. 2.6e-103;
Matches 216; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPPS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPPS 146

Qy   121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy   181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
              ||||||||||||||||||||||||||||||||||||
Db   207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 2
AAW38414
ID   AAW38414 standard; Protein; 288 AA.
XX
AC   AAW38414;
XX
DT   08-APR-1998 (first entry)

XX
DE   B7-1.
XX
KW   Screening; inhibitor; enhancer; binding; CD28; B7-1.
XX
OS   Homo sapiens.
XX
PN   EP795554-A2.
XX
PD   17-SEP-1997.
XX
PF   04-MAR-1997;   97EP-0301438.
XX
PR   02-OCT-1996;   96JP-0262085.
PR   05-MAR-1996;   96JP-0047795.
XX
PA   (TAKE) TAKEDA CHEM IND LTD.
XX
PI   Hattori M, Hida T, Kurokawa T, Nakanishi A;
XX
DR   WPI; 1997-450803/42.
DR   N-PSDB; AAT96358.
XX
PT   New xanthene derivatives useful as immunomodulators - e.g. methyl
PT   2-(carboxymethylsulphinyl)-5,7-dichloro-3,8-dihydroxy-6-"
PT   methyl-9-oxo-9H-xanthene-1-carboxylate.
XX
PS   Disclosure; Fig 4; 117pp; English.
XX
CC   The present sequence was used in the development of a novel method
CC   for screening for compounds that inhibit or enhance binding of CD28
CC   to B7-1.
XX
SQ   Sequence   288 AA;

Query Match   100.0%; Score 1149; DB 18; Length 288;
Best Local Similarity   100.0%; Pred. No. 2.6e-103;
Matches 216; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPPS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPPS 146

Qy   121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy   181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
              ||||||||||||||||||||||||||||||||||||
Db   207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 3
AAW67804
ID   AAW67804 standard; Protein; 288 AA.
XX
AC   AAW67804;
XX
DT   13-APR-1999 (first entry)
XX
DE   Human B7 protein sequence.
XX
KW   Human; B7; transfection; mammal; tumour cell; sarcoma; co-stimulation;
KW   T- cell; CD28; CTLA4; ligand; T-lymphocyte response; metastasis.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..34

Left column:

```
FT
FT   Protein        35..288
FT                  /note= "signal peptide"
FT   Domain         35..242
FT                  /note= "mature B7 protein"
FT   Domain         243..269
FT                  /note= "extracellular domain"
FT   Domain         270..288
FT                  /note= "transmembrane domain"
FT   Domain         ...
FT                  /note= "intracellular domain"
FT   Modified-site  53..55
FT                  /note= "Asn is N-glycosylated"
FT   Modified-site  89..91
FT                  /note= "Asn is N-glycosylated"
FT   Modified-site  98..100
FT                  /note= "Asn is N-glycosylated"
FT   Modified-site  186..188
FT                  /note= "Asn is N-glycosylated"
FT   Modified-site  207..209
FT                  /note= "Asn is N-glycosylated"
FT   Modified-site  211..213
FT                  /note= "Asn is N-glycosylated"
FT   Modified-site  226..228
FT                  /note= "Asn is N-glycosylated"
FT   Modified-site  236..234
FT                  /note= "Asn is N-glycosylated"
FT   Domain         35..139
FT                  /note= "Ig V-set domain"
FT   Domain         140..236
FT                  /note= "Ig C-set domain"
XX
PN   US5858776-A.
XX
PD   12-JAN-1999.
XX
PF   03-NOV-1993;    93US-0147772.
PR   03-NOV-1993;    93US-0147772.
XX
PA   (DAND )  DANA FARBER CANCER INST INC.
PA   (HARD )  HARVARD COLLEGE.
PA   (REPK )  REPLIGEN CORP.
XX
PI   Baskar S, Freeman GJ, Glimcher LH, Nadler LM, Ostrand-Rosenberg S;
XX
DR   WPI; 1999-119893/10.
DR   N-PSDB; AAX00757.
XX
PT   New modified tumour cells - transfected in order to express a T cell
PT   costimulatory molecule which allows the induction of an anti-tumour
PT   response by T cells
XX
PS   Disclosure; Column 31-34; 24pp; English.
XX
CC   This sequence represents the amino acid sequence of a human B7 protein.
CC   The coding sequence can be used to transfect mammalian tumour (sarcoma)
CC   cell so that the B7 protein is expressed by the tumour cell and has the
CC   ability to co-stimulate T cells and bind CD28 or CTLA4 ligand.
CC   The modified tumour cells can be used for inducing an anti-tumour
CC   T-lymphocyte response in a subject and are effective against both
CC   modified and unmodified tumour cells. The modified tumour cells can
CC   also be administered to prevent or inhibit metastatic spread of a tumour
CC   or to prevent or inhibit recurrence of a tumour following therapeutic
CC   treatment.
XX
SQ   Sequence     288 AA;

Query Match     100.0%;  Score 1149;  DB 20;  Length 288;
Best Local Similarity   100.0%;
Matches  216;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86
```

Right column:

```
Qy   61  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPPS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPPS 146

Qy  121  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||||||||||||||||||||||||||||||||
Db  207  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 4
AAW73640
ID   AAW73640 standard; Protein; 288 AA.
XX
AC   AAW73640;
XX
DT   23-MAR-1999  (first entry)
XX
DE   Human B7-2 antigen.
XX
KW   B7-2 antigen; mammalian tumour cell; T cell costimulation; CD28 ligand;
KW   CTLA4 ligand; therapy; T-cell response; human.
XX
OS   Homo sapiens.
XX
PN   US5861310-A.
XX
PD   19-JAN-1999.
XX
PF   30-MAY-1995;   95US-0456104.
PR   30-MAY-1995;   95US-0456104.
PR   03-NOV-1993;   93US-0147773.
XX
PA   (DAND )  DANA FARBER CANCER INST INC.
XX
PI   Freeman GJ, Gray GS, Nadler LM;
XX
DR   WPI; 1999-130394/11.
DR   N-PSDB; AAV55786.
XX
PT   Tumour cell transfected to express B7-2 molecule - useful for tumour
PT   therapy by stimulating T-cell response
XX
PS   Disclosure; Column 37-40; 27pp; English.
XX
CC   This sequence is the human B7-2 antigen, which can be used in the
CC   method of the invention. The method is for transfecting an isolated
CC   mammalian tumour cell with an exogenous nucleic acid molecule encoding a
CC   mammalian B7-2 molecule, where the B7-2 molecule is expressed in the
CC   tumour cell is capable of costimulating a T cell and is capable of
CC   binding a CD28 or CTLA4 ligand. The method is useful for treating tumours
CC   by stimulating a T-cell response against tumour cells in vivo.
XX
SQ   Sequence     288 AA;

Query Match     100.0%;  Score 1149;  DB 20;  Length 288;
Best Local Similarity   100.0%;
Matches  216;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy  121  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206
               |||||||||||||||||||||||||||||||||||
Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
               ||||||||||||||||||||||||||||||||||||
Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
```

RESULT 5

```
ID   AAB37087 standard; Protein; 288 AA.
AC   AAB37087;
DT   28-MAR-2001 (first entry)
DE   Human B lymphocyte antigen B7-1.
KW   Immunomodulator; fusion protein; human; murine; mouse; lymphocyte; CD28;
KW   antigen; extracellular domain; CTLA4; immunoglobulin constant region;
KW   immunogenicity; tumour; sarcoma; antigen presenting cell; macrophage;
KW   T cell-mediated immune response; transplantation; vaccination.
OS   Homo sapiens.
PN   US6130316-A.
PD   10-OCT-2000.
PF   26-JUL-1994;  94US-0280757.
PR   26-JUL-1993;  93US-0101624.
PR   19-AUG-1993;  93US-0109393.
PR   03-NOV-1993;  93US-0147773.
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (REPK ) REPLIGEN CORP.
PI   Freeman GJ, Nadler LM, Gray GS, Greenfield E;
DR   WPI; 2000-655681/63.
DR   N-PSDB; AAC84051.
PT   Nucleic acids and fusion proteins of CTLA4/CD28 ligands, useful for
PT   enhancing or suppressing T cell-mediated immune responses, especially
PT   during tissue, skin or organ transplantation, or in graft-versus-host
PT   disease -
```

PS   Disclosure; Column 87-90; 83pp; English.

```
CC   The invention relates to an isolated nucleic acid molecule encoding a
CC   fusion protein comprising a first nucleotide sequence encoding a first
CC   peptide, and a second nucleotide sequence encoding a second peptide.
CC   The first nucleotide sequence hybridizes in 6 X sodium chloride/sodium
CC   citrate (SSC) at 45 deg. C, followed by a wash in 0.2 X SSC at 50 deg. C
CC   to a portion of a nucleotide sequence which encodes a human or murine
CC   B lymphocyte antigen (B7-2) extracellular domain. The first peptide has
CC   the ability to bind CD28 or CTLA4. The first peptide has an amino acid
CC   sequence that is identical to at least 50% identical with the
CC   extracellular domain of a human B7-2 peptide (AAB37085). The second
CC   peptide is especially an immunoglobulin constant region. This sequence
CC   represents the human B lymphocyte antigen B7-1. The sequence is used for
CC   comparison with the B7-2 sequence. The human B7-2 protein is an example
CC   of a first peptide sequence of the invention. The nucleic acid molecules
CC   are useful in various expression vectors to direct synthesis of the
CC   corresponding proteins or peptides in a variety of hosts, particularly
CC   eukaryotic cells, e.g. mammalian or insect cell culture. The nucleic
CC   acids are also useful for enhancing the immunogenicity of a mammalian
CC   cell, e.g. tumour cell (sarcoma) or an antigen presenting cell
CC   (macrophage). The fusion proteins or peptides are useful for enhancing or
CC   suppressing T cell-mediated immune responses, e.g. in situations of
CC   tissue, skin or organ transplantation, or in graft-versus-host disease.
CC   The proteins are also useful for enhancing the efficacy of vaccination
CC   against a variety of pathogens, and may also be used to upregulate an
CC   immune response against a particular pathogen during an infection or
CC   against a tumour in a tumour-bearing host.
SQ   Sequence 288 AA;
```

```
Qy   Query Match             100.0%;  Score 1149;  DB 21;  Length 288;
Qy   Best Local Similarity   100.0%;  Pred. No. 2.6e-103;
     Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||||||||||||||||||||||||||||||||
Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
```

RESULT 6

```
ID   AAY99966 standard; Protein; 288 AA.
AC   AAY99966;
DT   10-JAN-2001 (first entry)
DE   Human B7 protein.
KW   B7; human; B cell activation antigen; B lymphocytes;
KW   autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW   herpes simplex; influenza; common cold; HIV.
OS   Homo sapiens.
```

```
FH   Key             Location/Qualifiers
FT   Domain          1..34
FT                   /label= "Ig V-set domain"
FT   Peptide         1..34
FT                   /label= Extracellular_domain
FT   Domain          35..138
FT                   /label= signal_peptide
FT   Domain          35..242
FT                   /label= "Ig C-set domain"
FT   Modified-site   53..55
FT                   /note= "N-linked glycosylation site"
FT   Modified-site   89..91
FT                   /note= "N-linked glycosylation site"
FT   Modified-site   98..100
FT                   /note= "N-linked glycosylation site"
FT   Domain          139..236
FT                   /label= "Ig C-set domain"
FT   Modified-site   186..188
FT                   /note= "N-linked glycosylation site"
FT   Modified-site   207..209
FT                   /note= "N-linked glycosylation site"
FT   Modified-site   211..213
FT                   /note= "N-linked glycosylation site"
FT   Modified-site   226..228
FT                   /note= "N-linked glycosylation site"
FT   Modified-site   232..234
FT                   /note= "N-linked glycosylation site"
FT   Domain          243..269
FT                   /label= Transmembrane_domain
FT   Domain          270..288
FT                   /label= Intracellular_domain
```

PN   US6071716-A.
XX
PD   06-JUN-2000.
XX
PF   15-NOV-1993;   93US-0153262.
XX
PR   28-AUG-1991;   91US-0751306.
PR   01-OCT-1990;   90US-0591300.
XX
PA   (DAND) DANA FARBER CANCER INST INC.
XX
PI   Nadler LM, Freeman GJ, Freedman AS;
XX
DR   WPI; 2000-422081/36.
DR   N-PSDB; AAA61328.
XX
PT   New polynucleotides encoding a B7 activation antigen, useful for
     regulating T cell mediated immune responses or viral diseases -
XX
PS   Claim 1; Fig.4; 36pp; English.
XX
CC   The present sequence is the unique human B cell activation antigen B7
CC   protein. The cDNA encoding this sequence was isolated from a Burkitt
CC   lymphoma cell line cDNA library. Selection of cDNA clones was based
CC   on expression of B7, as detected by the anti-B7 monoclonal antibody.
CC   The human B7 cDNA was used in hybridisation analysis to isolate the
CC   murine B7 cDNA (see AAA61329). The B7 nucleic acid sequences may be
CC   used to generate transgenic, knock-out animals which, in turn, are
CC   useful in the development and screening of therapeutically useful
CC   reagents. The expressed B7 protein is useful for enhancing or
CC   blocking activated T cell mediated immune responses and immune
CC   function. Modification of B7 expression is useful in the treatment of
CC   autoimmune diseases (e.g. rheumatoid arthritis or multiple sclerosis),
CC   herpes simplex, influenza, the common cold and HIV. It is also useful
CC   in tissue and organ transplantation.
XX
SQ   Sequence   288 AA;

Query Match   100.0%; Score 1149; DB 21; Length 288;
Best Local Similarity   100.0%; Pred. No. 2.6e-103;
Matches 216; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy   121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy   181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
              ||||||||||||||||||||||||||||||||||||
Db   207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 7
AAY44289
ID   AAY44289 standard; Protein; 288 AA.
XX
AC   AAY44289;
XX
DT   29-FEB-2000 (first entry)
XX
DE   Human B7.1 co-stimulatory molecule.
XX
KW   Human B7.1 co-stimulatory molecule; antigen presenting cell;
KW   immune response; cell surface receptor; Major histocompatibility complex;
KW   MHC classII; proton motor force; mitochondrial membrane potential;
KW   mitochondrial metabolism; cancer; autoimmune disease; glycoprotein;
KW   neurodegenerative disorder.
XX
OS   Homo sapiens.
XX
PN   WO9953953-A2.
XX
PD   28-OCT-1999.
XX
PF   30-MAR-1999;   99WO-US06874.
XX
PR   17-APR-1998;   98US-0082250.
PR   29-JUL-1998;   98US-0094519.
PR   24-SEP-1998;   98US-0101580.
XX
PA   (UIVE-) UNIV VERMONT.
XX
PI   Newell MK;
XX
DR   WPI; 2000-096773/08.
DR   N-PSDB; AA229320.
XX
PT   Disclosure; Page 115; 123pp; English.
XX
CC   The present sequence is human B7.1 co-stimulatory molecule. This is
CC   a glycoprotein on the surface of antigen presenting cells. This is
CC   involved in stimulation of an immune response by its ability to interact
CC   with various immune cell surface receptors. The regulation of cell
CC   surface expression of MHC classII and co-stimulatory molecule B7 can be
CC   manipulated by regulating the intracellular dissipation of proton motor
CC   force which can be assessed in terms of mitochondrial membrane potential.
CC   These methods can be used for regulating cell growth and division to
CC   control disease processes by manipulating mitochondrial metabolism and
CC   the expression of cell surface immune proteins. They can be used for
CC   treating diseases associated with excessive cellular division, aberrant
CC   differentiation, and premature cellular death, e.g. cancers, autoimmune
CC   diseases, neurodegenerative disorders etc.
XX
PS   Use of cell surface and membrane characteristics for developing
     products for treating cancers, autoimmune diseases or neurodegenerative
     diseases -
XX
SQ   Sequence   288 AA;

Query Match   100.0%; Score 1149; DB 21; Length 288;
Best Local Similarity   100.0%; Pred. No. 2.6e-103;
Matches 216; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy   121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy   181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
              ||||||||||||||||||||||||||||||||||||
Db   207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 8
AAY54920
ID   AAY54920 standard; Protein; 288 AA.
XX
AC   AAY54920;
XX
DT   14-FEB-2000 (first entry)
XX
DE   Human B7.1 protein sequence.

XX
KW   Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;
KW   IL-12 p40 subunit; gene therapy; tumour; leukaemia; B7.1 protein.
XX
OS   Homo sapiens.
XX
PN   US5994104-A.
XX
PD   30-NOV-1999.
XX
PF   08-NOV-1996;   96US-0751767.
XX
PR   08-NOV-1996;   96US-0751767.
XX
PA   (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.
XX
PI   Anderson RJ, Prentice HG, MacDonald ID;
XX
DR   WPI; 2000-038261/03.
DR   N-PSDB; AAZ40022.
XX
PS   Example: Fig 10; 73pp; English.
XX
PT   Nucleic acid constructs encoding interleukin-12 fusion proteins useful
PT   for treating leukemia and other cancers -
XX
CC   This sequence represents the human B7.1 protein sequence.
CC   The invention relates to an isolated nucleic acid construct (I)
CC   comprising a region encoding an interleukin-12 (IL-12) fusion protein
CC   (comprising a region encoding an IL-12 p35 subunit, an IL-12 p40
CC   peptide (joining the subunits)) and a region encoding a B7 protein. (I)
CC   may be used to produce IL-12 fusion proteins according to standard
CC   recombinant DNA methodologies. The fusion proteins may be produced either
CC   in vitro in a fermentation culture or in vivo as part of a gene therapy
CC   protocol (in this case (I) is used to transform a patients cells, which
CC   then secrete the functional polypeptide to supplement the patients own
CC   production of IL-12 or to rectify mutations which lead to the production
CC   of inactive polypeptides). The fusion proteins produced in this way may
CC   be used to treat any disease which responds to IL-12 such as tumours
CC   (both solid and dispersed of the kidney, breast, colon, ovarian and
CC   cervical tumours and melanomas) and in particular, tumours of the blood
CC   such as leukaemia. Alternatively, the polypeptides may be used as
CC   antigens in the production of antibodies to IL-12 and to assay for
CC   agonists and antagonists of its activity. The antibodies and antagonists
CC   may be used to inhibit the activity of IL-12. (I) may also be used
CC   diagnostically as a probe which hybridizes to sequences encoding IL-12
CC   and the antibodies may be used to detect the presence of IL-12
CC   polypeptides in samples. They may be used diagnostically to quantitate
CC   the expression of the polypeptide by patients and hence which subjects
CC   may be in need of restorative therapy.
XX
SQ   Sequence   288 AA;

Query Match   100.0%; Score 1149; DB 21; Length 288;
Best Local Similarity   100.0%; Pred. No. 2.6e-103;
Matches 216; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSCGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSCGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
        ||||||||||||||||||||||||||||||||||||
Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
```

RESULT 9
AAU05121
ID   AAU05121 standard; Protein; 288 AA.
XX
AC   AAU05121;
XX
DT   24-OCT-2001 (first entry)
XX
DE   Colorectal tumour antigen CD80.
XX
KW   Colorectal cancer; immunostimulant; cytostatic; immune response;
KW   adenocarcinoma; allogeneic tumour cell; SW620 cell; COLO 205 cell;
KW   SW403 cell; colon; breast; lung; prostate; cancer; vaccine;
KW   tumour antigen CD80.
XX
OS   Homo sapiens.
XX
PN   WO200154716-A2.
XX
PD   02-AUG-2001.
XX
PF   26-JAN-2001;   2001WO-US02731.
PR   27-JAN-2000;   2000US-0178498.
PR   28-FEB-2000;   2000US-0185335.
XX
PA   (KIMM-) KIMMEL CANCER CENT SIDNEY.
PA   (IMMU-) IMMUNE RESPONSE CORP.
XX
PI   Sobol RE, Shawler DL, Bartholomew RM, Carlo DJ, Gold DP;
XX
DR   WPI; 2001-502616/55.
DR   N-PSDB; AAS11426.
XX
PS   Example 2; Page 130-131; 131pp; English.
XX
PT   New composition comprising an allogeneic tumour cell, useful for
PT   stimulating an immune response in a patient having an adenocarcinoma,
PT   especially useful for treating colorectal, breast, lung or prostate
PT   cancer -
XX
CC   The invention relates to a composition for stimulating an immune response
CC   in a patient having an adenocarcinoma or colorectal cancer. The
CC   composition comprises an allogeneic tumour cell selected from SW620 cell,
CC   COLO 205 cell and SW403 cell, and a physiological carrier. The allogeneic
CC   cell stimulates an immune response to an autologous tumour cell in the
CC   patient. The composition is useful for stimulating an immune response in
CC   a patient having an adenocarcinoma, e.g. colon, breast, lung or prostate
CC   adenocarcinoma. The use of allogeneic tumour cells provides a generic
CC   source of antigen that can be administered to a variety of patients, in
CC   contrast to using autologous tumour cells, which must be isolated from
CC   each individual patient. The allogeneic cells are suitable as a cancer
CC   vaccine and can stimulate an immune response against autologous tumour
CC   cells of a cancer patient. The present sequence represents the amino acid
CC   sequence of colorectal tumour antigen CD80 used in the method of the
CC   invention.
XX
SQ   Sequence   288 AA;

Query Match   100.0%; Score 1149; DB 22; Length 288;
Best Local Similarity   100.0%; Pred. No. 2.6e-103;
Matches 216; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
```

Db
Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||||||||||||||||||||||||||||||||
Db 207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 10
ID   AAB19959 standard; Protein; 288 AA.
AC   AAB19959;
DT   19-MAR-2001 (first entry)
DE   Human B lymphocyte antigen B7.
XX
KW   Human; B7; B lymphocyte; antigen; T cell costimulatory molecule;
KW   CD28; CTLA4; tumour; melanoma; neuroblastoma; leukaemia; carcinoma;
KW   metastasis; antitumour; therapy.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   Peptide   1..34
FT   /label= Signal_peptide
FT   Protein   35..288
FT   /label= Mature_protein
FT   Domain   35..242
FT   /note= "extracellular domain"
FT   Domain   243..269
FT   /note= "transmembrane domain"
FT   Domain   270..288
FT   /note= "intracellular domain"
FT   Domain   35..138
FT   /note= "immunoglobulin V-set domain"
FT   Domain   139..236
FT   /note= "immunoglobulin C-set domain"
FT   Modified-site   53..55
FT   /note= "Asn is N-glycosylated"
FT   Modified-site   89..91
FT   /note= "Asn is N-glycosylated"
FT   Modified-site   98..100
FT   /note= "Asn is N-glycosylated"
FT   Modified-site   186..188
FT   /note= "Asn is N-glycosylated"
FT   Modified-site   207..209
FT   /note= "Asn is N-glycosylated"
FT   Modified-site   211..213
FT   /note= "Asn is N-glycosylated"
FT   Modified-site   226..228
FT   /note= "Asn is N-glycosylated"
FT   Modified-site   232..234
FT   /note= "Asn is N-glycosylated"
XX
PS   Claim 4; Column 31-34; 24pp; English.
XX
PT   Modifying tumor cell for treating tumors, reducing metastatic spread,
PT   inhibiting recurrence of tumor and increasing immunogenicity, involves
PT   transfecting tumor cells with a nucleic acid encoding B7 molecule -
XX
CC   The present sequence is that of human lymphocyte antigen B7, a T
CC   cell costimulatory molecule that binds to CD28 and CTLA4. Tumour
CC   cells modified to express a T cell costimulatory molecule,
CC   especially B7, are disclosed. The tumour cells are modified by
CC   transfection with a nucleic acid encoding the T cell costimulatory
CC   molecule, by using an agent which induces or increases expression
CC   of the T cell costimulatory molecule on the tumour cell surface, or
CC   by coupling the T cell costimulatory molecule to the tumour cell
CC   surface. Tumour cells further modified to express major
CC   histocompatibility complex (MHC) class I and/or class II molecules,
CC   or in which expression of an MHC associated protein, the invariant
CC   chain, is inhibited are also disclosed. The modified tumour cells
CC   are used to treat a patient with a tumour, preventing or inhibiting
CC   metastatic spread or tumour recurrence. The tumour may be a
CC   melanoma, a neuroblastoma, a leukaemia or a carcinoma. A method for
CC   specifically inducing a CD4+ T cell response against a tumour, and a
CC   method for treating a tumour by modification of tumour cells in vivo
CC   are also disclosed. The treatment methods increase the immunogenicity
CC   of the tumour cell in vivo. The antitumour T cell-mediated immune
CC   response is effective both against the modified tumour cells and the
CC   unmodified tumour cells from which the modified cells were derived.
CC   Thus, the effector phase of the antitumour response induced by the
CC   modified tumour cells is not dependent upon expression of a
CC   costimulatory molecule on the tumour cells.
XX
SQ   Sequence   288 AA;

Query Match   100.0%; Score 1149; DB 22; Length 288;
Best Local Similarity   100.0%;
Matches 216; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIPDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADPFTPS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIPDIINNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADPFTPS 146

Qy 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||||||||||||||||||||||||||||||||
Db 207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 11
ID   AAW41415 standard; Protein; 473 AA.
AC   AAW41415;
DT   02-JUN-1998 (first entry)
DE   Human B7.1-murine A5B7 F(ab')2 fusion protein.
XX
KW   Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
KW   cancer diagnosis; complementarity determining region.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Mus sp.
XX
PN   WO9742329-A1.
XX

PI   Baskar S, Glimcher LH, Freeman GJ, Ostrand-Rosenberg S;
PI   Nadler LM;
XX
PA   (HARD) HARVARD COLLEGE.
PA   (DAND) DANA FARBER CANCER INST INC.
PA   (GEMY) GENETICS INST INC.
XX
PR   03-NOV-1993; 93US-0147772.
PN   US6149905-A.
PD   21-NOV-2000.
PF   23-SEP-1998; 98US-0159135.
XX
DR   N-PSDB; AAA89224.
DR   WPI; 2001-079388/09.

```
PD   13-NOV-1997.
XX
PF
XX
PR   29-APR-1997;   97WO-GB01165.
XX
PR   14-FEB-1997;   97GB-0003103.
PR   04-MAY-1996;   96GB-0009405.
XX
PA   (ZENE ) ZENECA LTD.
XX
PI   Copley CG, Edge MD, Emery SC;
XX
DR   WPI; 1997-558987/51.
DR   N-PSDB; AAV17340.
XX
PT   Anti-carcinoembryonic antigen antibody 806.077 Ab - used for
PT   diagnosis and therapy of cancer.
XX
PS   Reference Example 3; Page 190-193; 208pp; English.
XX
CC   This sequence is the human B7.1-murine A5B7 F(ab')2 fusion protein
CC   (AB7), and is an example of the antibody of the invention. The antibody
CC   is an anti-CEA (carcinoembryonic antigen) antibody (preferably
CC   806.077 Ab). Host cells or transgenic organisms transformed with DNA
CC   encoding the antibody, are used to make the antibody or conjugate. The
CC   conjugate is used in a medicament suitable for intravenous
CC   administration. The conjugate can be used for cancer therapy, selectively
CC   killing tumour cells. The antibody can be used for in vivo or in vitro
CC   diagnosis of cancer.
XX
SQ   Sequence    473 AA;

Query Match          100.0%;   Score 1149;   DB 18;   Length 473;
Best Local Similarity 100.0%;   Pred. No. 5.3e-103;
Matches 216;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELIYAVSSKLDF 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELIYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||||||||||||||||||||||||||||||||
Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 12
ID   AAW90208 standard; Protein; 251 AA.
XX
AC   AAW90208;
XX
DT   10-MAY-1999 (first entry)
XX
DE   hB7.1glu-glu soluble fusion protein.
XX
KW   B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
KW   CD86; T cell activation; inhibitor; graft versus host disease;
KW   transplant rejection; allograft rejection; autoimmune disease;
KW   allergy; therapy; human; hB7.1glu-glu.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - synthetic.
XX
KW
FH   Key             Location/Qualifiers
FT   Peptide         1..34
FT                   /note= "potential eukaryotic secretory signal
```

```
FT   Domain          35..242
FT                   /note= "human B7.1 (mature protein) extracellular
FT                   domain"
FT   Peptide         243..251
FT                   /note= "Glu-Glu detection/purification tag"
XX
PN   WO9858965-A2.
XX
PD   30-DEC-1998.
XX
PF   22-JUN-1998;   98WO-EP03791.
XX
DR   20-JUN-1997;   97EP-0870092.
XX
PI   Bosman A, Buyse M, Lorre K, Sablon E;
XX
PA   (INNO-) INNOGENETICS NV.
XX
PS   Example 3.1.2; Fig 4; 182pp; English.
XX
CC   This 29 kDa soluble fusion protein, termed hB7.1glu-glu, is composed
CC   of human co-stimulatory molecule B7.1 extracellular domain fused
CC   C-terminally to a synthetic Glu-Glu epitope (see AAW90197). It
CC   was produced from total RNA of Epstein-Barr virus-transformed
CC   human spleen cells by RT-PCR using primers MR67 and MR145 (see
CC   AAX01601). The fusion protein has been produced in Sf9 Spodoptera
CC   frugiperda insect cells using a baculovirus expression system.
CC   The invention relates to molecules such as diabodies, trivalent and
CC   tetravalent antibodies and small antigen binding peptides which can
CC   cross-link, or cross-react with, B7.1 and B7.2 expressed on
CC   professional antigen presenting cells leading to the inhibition of
CC   antigen-specific T cell activation. Methods to produce such
CC   molecules are provided. The molecules are used to treat or prevent
CC   diseases of the immune system, in particular graft rejection, graft
CC   versus host disease, allergy and autoimmune diseases (claimed).
XX
SQ   Sequence    251 AA;

Query Match          99.7%;   Score 1146;   DB 20;   Length 251;
Best Local Similarity 99.5%;   Pred. No. 4.2e-103;
Matches 215;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELIYAVSSKLDF 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELIYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         |||||||||||||||||||||||||||||||:||||
Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 13
ID   AAW38415 standard; Protein; 475 AA.
XX
AC   AAW38415;
XX
DT   08-APR-1998 (first entry)
XX
```

```
DE   Soluble B7-1-Ig.
XX
KW   Screening; inhibitor; enhancer; binding; CD28; B7-1;
KW   soluble B7-1-Ig; immunoglobulin.
XX
OS   Homo sapiens.
XX
PN   EP795554-A2.
XX
PD   17-SEP-1997.
XX
PF   04-MAR-1997;   97EP-0301438.
XX
PR   02-OCT-1996;   96JP-0262085.
PR   05-MAR-1996;   96JP-0047795.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Hattori M, Hida T, Kurokawa T, Nakanishi A;
XX
DR   WPI; 1997-450803/42.
DR   N-PSDB; AAT96359.
XX
PT   New xanthene derivatives useful as immunomodulators - e.g. methyl
PT   2-(carboxymethylsulphinyl)-5,7-dichloro-3,8-dihydroxy-6-
PT   methyl-9-oxo-9H-xanthene-1-carboxylate.
PS   Disclosure; Fig 6 and 7; 117pp; English.
CC   The present sequence was used in the development of a novel method
CC   for screening for compounds that inhibit or enhance binding of CD28
CC   to B7-1.
XX
SQ   Sequence    475 AA;

Query Match             99.6%;  Score 1144;   DB 18;   Length 475;
Best Local Similarity   99.5%;  Pred. No. 1.6e-102;
Matches  215;  Conservative   1;  Mismatches   0;  Indels    0;  Gaps    0;

Qy      1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy     61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy    121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy    181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
          |||||||||||||||||||||||||||||||||||:
Db    207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDH 242

RESULT 14
AAW86004
ID   AAW86004 standard; Protein; 488 AA.
XX
AC   AAW86004;
XX
DT   15-MAR-1999  (first entry)
XX
DE   Human B7-1.5T4.1 protein fusion, specific for human 5T4.
XX
KW   Tumour interacting protein; cancer; gene therapy; vector;
KW   5T4 antigen; monoclonal antibody; single chain antibody;
KW   mouse; human; B7-1; co-stimulatory molecule.
XX
OS   Chimeric - Mus sp.
OS   Chimeric - Homo sapiens.
OS   Chimeric - synthetic.
```

```
XX
PN   WO9855607-A2.
XX
PD   10-DEC-1998.
XX
PF   04-JUN-1998;   98WO-GB01627.
XX
PR   04-JUL-1997;   97GB-0014230.
PR   04-JUN-1997;   97GB-0011579.
PR   20-JUN-1997;   97GB-0013150.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Bebbington CR, Carroll MW, Ellard FM, Kingsman SM;
PI   Myers KA;
XX
DR   WPI; 1999-059910/05.
DR   N-PSDB; AAV80292.
XX
PT   New vector encoding a tumour interacting protein for treating cancer
PT   - contains a desired nucleotide sequence and/or protein which
PT   recognises tumours, and is used as a gene delivery system to treat
PT   cancer
XX
PS   Example 5; Fig 2; 82pp; English.
XX
CC   This is the amino acid sequence of B7-1.5T4.1, a fusion protein
CC   comprising the extracellular domain (amino acids 1-215) of human
CC   co-stimulatory molecule B7-1 joined via a flexible peptide linker
CC   to an scFv (see AAW86002) derived from murine 5T4 monoclonal
CC   antibody.  B7-1.5T4.1 cDNA (see AAV80292) can be inserted into vector
CC   pCI to allow expression of the fusion protein in mammalian cells.
CC   The trophoblast cell surface antigen defined by 5T4 is expressed at
CC   high levels on the cells of a wide variety of human tumours.  The
CC   invention relates to a vector comprising a nucleotide sequence
CC   coding for a tumour interacting protein (TIP) and optionally a
CC   nucleotide sequence of interest (NOI), which encodes a protein of
CC   interest (POI), the vector being capable of delivering the NOI
CC   and/or POI to the tumour recognised by the TIP.  Delivery can be in
CC   vivo or ex vivo.  The vector is used to treat cancer, and may also
CC   used as a gene delivery system for introducing at least 1 gene
CC   encoding a TIP (preferably a tumour binding protein) into a
CC   haematopoietic cell lineage.  B7-1 is expected to bind specifically
CC   to CD28 and CTLA-4 present on human T-cells.
XX
SQ   Sequence    488 AA;

Query Match             99.5%;  Score 1143;   DB 20;   Length 488;
Best Local Similarity   100.0%;  Pred. No. 2.1e-102;
Matches  215;  Conservative   0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy      1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy     61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy    121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy    181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPD 215
          |||||||||||||||||||||||||||||||||||
Db    207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPD 241

RESULT 15
AAB83836
ID   AAB83836 standard; Protein; 488 AA.
XX
AC   AAB83836;
```

```
XX
DT   23-JUL-2001  (first entry)
XX
DE   Amino acid sequence of a B7-1.5T4.1 fusion protein.
XX
KW   Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
KW   hypersensitivity; autoimmune disease; central nervous system disorder;
KW   Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW   cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW   Helicobacter-related disease; immune disorder.
XX
OS   Synthetic.
OS   Mus sp.
OS   Homo sapiens.
XX
PN   WO200136486-A2.
XX
PD   25-MAY-2001.
XX
PF   13-NOV-2000; 2000WO-GB04317.
XX
PR   18-NOV-1999; 99WO-GB03859.
PR   15-FEB-2000; 2000GB-0003527.
PR   02-MAR-2000; 2000GB-0005071.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Kingsman A,  Kingsman SM,  Bebbington CR,  Carroll MW,  Ellard FM;
PI   Myers KA;
XX
DR   WPI; 2001-343805/36.
DR   N-PSDB; AAF89730.
XX
PT   Use of single chain antibody capable of recognizing a disease
PT   associated molecule for manufacturing a medicament for preventing
PT   and/or treating a disease condition associated with disease associated
PT   molecule -
XX
PS   Claim 3; Fig 2; 118pp; English.
XX
CC   The specification describes the use of a single chain antibody (ScFv),
CC   which is capable of recognizing a disease associated molecule in the
CC   manufacture of a medicament for the prevention and treatment of a
CC   disease condition. The ScFv antibody is useful in the manufacture of
CC   a medicament, for affecting a disease in vivo, for preparing a
CC   pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC   treatment of a disease. The ScFv antibody is also useful for
CC   treating inflammatory diseases including arthritis, hypersensitivity,
CC   autoimmune diseases, cancers, central nervous system disorders
CC   including Parkinson's disease, periodontal diseases, cardiopulmonary
CC   diseases, cardiovascular diseases, gastrointestinal disorders,
CC   infections, diabetes, Helicobacter-related diseases, and other immune
CC   disorders. The present sequence represents a B7-1.5T4.1 fusion protein.
CC   This comprises the N-terminus of the 5T4 ScFv is fused after amino acid
CC   215 of human B7-1.
XX
SQ   Sequence  488 AA;

Query Match             99.58%;  Score 1143;  DB 22;  Length 488;
Best Local Similarity   100.0%;
Matches  215;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
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Db     27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy     61 YKNRTIFDITNNLSIVILALRSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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Db     87 YKNRTIFDITNNLSIVILALRSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy    121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy    181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPD 215
          |||||||||||||||||||||||||||||||||||
Db    207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPD 241

Search completed: October 17, 2002, 16:36:15
Job time : 33 secs
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OM protein - protein search, using sw model

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

Run on: October 17, 2002, 16:35:40 ; Search time 13 Seconds
(without alignments)
405.841 Million cell updates/sec

Title: US-09-454-651B-23
Perfect score: 1149
Sequence: 1 GLSHFCSGVIHVTKEVKEVA........LRVNQTFNWNTTKQEHFPDN 216
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	DB ID	Description
1	1149	100.0	288	2	US-08-147-772-2	Sequence 2, Appli
2	1149	100.0	288	2	US-08-456-104-6	Sequence 6, Appli
3	1149	100.0	288	2	US-08-101-624-23	Sequence 23, Appli
4	1149	100.0	288	2	US-08-751-767A-6	Sequence 6, Appli
5	1149	100.0	288	3	US-08-153-262-2	Sequence 2, Appli
6	1149	100.0	288	4	US-08-479-744A-29	Sequence 29, Appli
7	1149	100.0	288	4	US-08-280-757B-29	Sequence 29, Appli
8	1149	100.0	288	4	US-08-159-135-2	Sequence 2, Appli
9	1149	100.0	288	4	US-08-205-697A-19	Sequence 19, Appli
10	1149	100.0	288	4	US-08-702-525-19	Sequence 19, Appli
11	1149	100.0	288	4	US-09-450-798-2	Sequence 2, Appli
12	1149	100.0	288	4	US-08-403-253A-2	Sequence 2, Appli
13	1149	100.0	288	5	PCT-US95-02576-19	Sequence 19, Appl
14	1149	100.0	473	4	US-09-171-945-131	Sequence 131, App
15	1102	95.9	208	4	US-09-460-384-36	Sequence 36, Appli
16	1050	91.4	208	3	US-08-630-172-15	Sequence 15, Appli
17	1050	91.4	208	4	US-09-375-419-15	Sequence 15, Appli
18	561	48.8	306	4	US-08-205-697A-17	Sequence 17, Appli
19	561	48.8	306	4	US-08-702-525-17	Sequence 17, Appli
20	561	48.8	306	4	PCT-US95-02576-17	Sequence 17, Appl
21	561	48.8	320	4	US-08-205-697A-2	Sequence 2, Appli
22	561	48.8	320	4	US-08-702-525-2	Sequence 2, Appli
23	561	48.8	320	5	PCT-US95-02576-2	Sequence 2, Appl
24	558	48.6	306	5	US-08-147-772-4	Sequence 4, Appli
25	558	48.6	306	2	US-08-456-104-8	Sequence 8, Appli
26	558	48.6	306	2	US-08-101-624-25	Sequence 25, Appli
27	558	48.6	306	3	US-08-153-262-4	Sequence 4, Appli
28	558	48.6	306	3	US-08-479-744A-31	Sequence 31, Appl
29	558	48.6	306	4	US-08-280-757B-31	Sequence 31, Appl
30	558	48.6	306	4	US-09-159-135-4	Sequence 4, Appli
31	558	48.6	306	4	US-09-450-798-4	Sequence 4, Appli
32	311	27.1	200	4	US-08-205-697A-9	Sequence 9, Appli
33	311	27.1	200	5	US-08-702-525-9	Sequence 9, Appli
34	311	27.1	200	5	PCT-US95-02576-9	Sequence 9, Appl
35	311	27.1	214	4	US-08-205-697A-11	Sequence 11, Appli
36	311	27.1	214	4	US-08-702-525-11	Sequence 11, Appli
37	311	27.1	214	5	PCT-US95-02576-11	Sequence 11, Appl
38	250.5	21.8	212	4	US-08-702-525-63	Sequence 63, Appl
39	250.5	21.8	212	5	PCT-US95-02576-63	Sequence 63, Appl
40	250.5	21.8	226	4	US-08-702-525-65	Sequence 65, Appl
41	250.5	21.8	226	5	PCT-US95-02576-65	Sequence 65, Appl
42	182	15.8	323	5	US-08-702-525-2	Sequence 2, Appli
43	182	15.8	329	2	US-08-456-104-2	Sequence 2, Appli
44	182	15.8	329	2	US-08-101-624-2	Sequence 2, Appli
45	182	15.8	329	3	US-08-479-744A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-147-772-2
Sequence 2, Application US/08147772
Patent No. 5858776
GENERAL INFORMATION:
   APPLICANT: Ostrand-Rosenberg, Suzanne
   APPLICANT: Baskar, Sivasubramanian
   APPLICANT: Glimcher, Laurie H.
   APPLICANT: Freeman, Gordon J.
   APPLICANT: Nadler, Lee M.
   TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
   NUMBER OF SEQUENCES: 4
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: LAHIVE & COCKFIELD
   STREET: 60 State Street, Suite 510
   CITY: Boston
   STATE: Massachusetts
   COUNTRY: USA
   ZIP: 02109
   COMPUTER READABLE FORM:
   MEDIUM TYPE: Floppy disk
   COMPUTER: IBM PC compatible
   OPERATING SYSTEM: PC-DOS/MS-DOS
   SOFTWARE: PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/08/147,772
   FILING DATE:
   CLASSIFICATION: 424
   PRIOR APPLICATION DATA:
   APPLICATION NUMBER:
   FILING DATE:
   ATTORNEY/AGENT INFORMATION:
   NAME: Mandragouras, Amy E.
   REGISTRATION NUMBER: 36,207
   REFERENCE/DOCKET NUMBER: RPI-003
   TELECOMMUNICATION INFORMATION:
   TELEPHONE: (617) 227-7400
   TELEFAX: (617) 227-5941
   INFORMATION FOR SEQ ID NO: 2:
   SEQUENCE CHARACTERISTICS:
   LENGTH: 288 amino acids
   TYPE: amino acid
   TOPOLOGY: linear
   MOLECULE TYPE: protein
   DESCRIPTION: B cell activation antigen; natural ligand
   DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
   FEATURE:
   NAME/KEY: signal sequence
   LOCATION: -34 to -1
   IDENTIFICATION METHOD: amino terminal sequencing of

IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
  NAME/KEY: extracellular domain
  LOCATION: 1 to 208
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: transmembrane domain
  LOCATION: 209 to 235
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: intracellular domain
  LOCATION: 236 to 254
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: N-linked glycosylation
  LOCATION: 19 to 21
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: N-linked glycosylation
  LOCATION: 173 to 175
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: N-linked glycosylation
  LOCATION: 152 to 154
  IDENTIFICATION METHOD: similarity with known
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  NAME/KEY: N-linked glycosylation
  LOCATION: 55 to 57
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: N-linked glycosylation
  LOCATION: 64 to 66
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: N-linked glycosylation
  LOCATION: 177 to 179
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: N-linked glycosylation
  LOCATION: 192 to 194
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: N-linked glycosylation
  LOCATION: 198 to 200
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: Ig C-set domain
  LOCATION: 105 to 202
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: Ig V-set domain
  LOCATION: 1 to 104
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence

PUBLICATION INFORMATION:
  AUTHORS: FREEMAN, GORDON J.
  AUTHORS: FREEDMAN, ARNOLD S.
  AUTHORS: SEGIL, JEFFREY M.
  AUTHORS: LEE, GRACE
  AUTHORS: WHITMAN, JAMES F.
  AUTHORS: NADLER, LEE M.
  TITLE: B7, A New Member Of The Ig Superfamily With
  TITLE: Unique Expression On Activated And Neoplastic B Cells
  JOURNAL: The Journal of Immunology
  VOLUME: 143
  ISSUE: 8
  PAGES: 2714-2722
  DATE: 15-OCT-1989
  RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-147-772-2

Query Match   100.0%; Score 1149; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPFTPS 120
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Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPFTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
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RESULT 2
US-08-456-104-6
Sequence 6, Application US/08456104
Patent No. 5861310
GENERAL INFORMATION:
  APPLICANT: Freeman, Gordon J.
  APPLICANT: Nadler, Lee M.
  APPLICANT: Gray, Gary S.
  TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE
  NUMBER OF SEQUENCES: 8
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: LAHIVE & COCKFIELD
    STREET: 60 State Street, Suite 510
    CITY: Boston
    STATE: Massachusetts
    COUNTRY: USA
    ZIP: 02109
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/456,104
    FILING DATE:
  PRIOR APPLICATION DATA:
    CLASSIFICATION: 424
    APPLICATION NUMBER: 08/101,624;
    FILING DATE: 26-JUL-1993;
    APPLICATION NUMBER: 08/109,393;
    FILING DATE: 19-AUG-1993
  ATTORNEY/AGENT INFORMATION:
    NAME: Mandragouras, Amy E.
    REGISTRATION NUMBER: 36,207
    REFERENCE/DOCKET NUMBER: RPI-008
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (617) 227-7400
    TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 288 amino acids

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      TYPE: amino acid
      TOPOLOGY: linear
      MOLECULE TYPE: protein
US-08-456-104-6

Query Match             100.0%;  Score 1149;  DB 2;  Length 288;
Best Local Similarity   100.0%;  Pred. No. 5.2e-113;
Matches 216;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
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Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242


RESULT 3
US-08-101-624-23
Sequence 23, Application US/08101624
Patent No. 5942607
GENERAL INFORMATION:
    APPLICANT: Freeman, Gordon J.
    APPLICANT: Nadler, Lee M.
    APPLICANT: Gray, Gary S.
    TITLE OF INVENTION: No. 5942607e1 CTLA4/CD28 Ligands and
    TITLE OF INVENTION: Uses Therefor
    NUMBER OF SEQUENCES: 25
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: LAHIVE & COCKFIELD
        STREET: 60 State Street, Suite 510
        CITY: Boston
        STATE: Massachusetts
        COUNTRY: USA
        ZIP: 02109
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: Patentin Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/101,624
        FILING DATE: 26-JUL-1993
        CLASSIFICATION: 514
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER:
        FILING DATE:
    ATTORNEY/AGENT INFORMATION:
        NAME: Mandragouras, Amy E.
        REGISTRATION NUMBER: 36,207
        REFERENCE/DOCKET NUMBER: RPI-004
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: (617) 227-7400
        TELEFAX: (617) 227-5941
    INFORMATION FOR SEQ ID NO: 23:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 388 amino acids
        TYPE: amino acid
        TOPOLOGY: linear
    MOLECULE TYPE: protein
    DESCRIPTION: B cell activation antigen; natural ligand
    DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
    FEATURE:
        NAME/KEY: signal sequence
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    FEATURE:
        NAME/KEY: extracellular domain
        LOCATION: 1 to 208
        IDENTIFICATION METHOD: similarity with known
    OTHER INFORMATION: hydrophobic
        LOCATION: -34 to -1
        IDENTIFICATION METHOD: amino terminal sequencing of
        IDENTIFICATION METHOD: soluble protein
    FEATURE:
        NAME/KEY: transmembrane domain
        LOCATION: 209 to 235
        IDENTIFICATION METHOD: sequence
    FEATURE:
        NAME/KEY: intracellular domain
        LOCATION: 236 to 254
        IDENTIFICATION METHOD: sequence
    FEATURE:
        NAME/KEY: N-linked glycosylation
        LOCATION: 19 to 21
        IDENTIFICATION METHOD: sequence
    FEATURE:
        NAME/KEY: N-linked glycosylation
        LOCATION: 55 to 57
        IDENTIFICATION METHOD: sequence
    FEATURE:
        NAME/KEY: N-linked glycosylation
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        NAME/KEY: N-linked glycosylation
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        NAME/KEY: N-linked glycosylation
        LOCATION: 173 to 175
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        NAME/KEY: N-linked glycosylation
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        IDENTIFICATION METHOD: sequence
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        NAME/KEY: N-linked glycosylation
        LOCATION: 198 to 200
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        NAME/KEY: Ig V-set domain
        LOCATION: 1 to 104
        IDENTIFICATION METHOD: similarity with known
        IDENTIFICATION METHOD: sequence
    FEATURE:
        NAME/KEY: Ig C-set domain
        LOCATION: 105 to 202
        IDENTIFICATION METHOD: similarity with known
        IDENTIFICATION METHOD: sequence
    PUBLICATION INFORMATION:
        AUTHORS: FREEMAN, GORDON J.
        AUTHORS: FREEDMAN, ARNOLD S.
        AUTHORS: SEGIL, JEFFREY M.
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AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 23: From -26 to 262

US-08-101-624-23

Query Match   100.0%;   Score 1149; DB 2;   Length 288;
Best Local Similarity 100.0%;   Pred. No. 5.2e-113;
Matches 216;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Db  27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  86

Qy  61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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Db  87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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Db 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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Db 207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
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RESULT 4
US-08-751-767A-6
Sequence 6, Application US/08751767A
Patent No. 5994104
GENERAL INFORMATION:
  APPLICANT: ANDERSON, ROBERT J.
  APPLICANT: GRANT, HUGH
  APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLEUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
  ADDRESSEE: NIXON & VANDERHYE P.C.
  STREET: 1100 NORTH GLEBE ROAD
  CITY: ARLINGTON
  STATE: VA
  COUNTRY: USA
  ZIP: 22201
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/751,767A
  FILING DATE: 08-NOV-1996
  CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
  NAME: SADOFF, B.J.
  REGISTRATION NUMBER: 36,663
  REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 703164100
  TELEFAX: 7038164091
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
  LENGTH: 288 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
  MOLECULE TYPE: protein

US-08-751-767A-6

Query Match   100.0%;   Score 1149; DB 2;   Length 288;
Best Local Similarity 100.0%;   Pred. No. 5.2e-113;
Matches 216;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Db  27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  86

Qy  61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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Db  87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
       ||||||||||||||||||||||||||||||||||||
Db 207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
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RESULT 5
US-08-153-262-2
Sequence 2, Application US/08153262
Patent No. 6071716
GENERAL INFORMATION:
  APPLICANT: FREEMAN, GORDON J.
  APPLICANT: FREEMAN, ARNOLD S.
  APPLICANT: NADLER, LEE M.
TITLE OF INVENTION: DNA Encoding B7, A New Member
TITLE OF INVENTION: Of The IgG Superfamily With Unique Expression On
TITLE OF INVENTION: Activated And Neoplastic B Cells.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
  ADDRESSEE: The Dana-Farber Cancer Institute
  STREET: 44 Binney Street
  CITY: Boston
  STATE: Massachusetts
  COUNTRY: U.S.A.
  ZIP: 02115
COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage
  COMPUTER: IBM Personal System 2; Model 30
  OPERATING SYSTEM: MS/DOS
  SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/153,262
  FILING DATE:
  CLASSIFICATION:
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/751,306
  FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
  NAME: HART, JULIA D.
  REGISTRATION NUMBER: 33132
  REFERENCE/DOCKET NUMBER: DFCI-116.1
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (203) 255-9900
  TELEFAX: (203) 259-2846
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
  LENGTH: 288 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
  MOLECULE TYPE: protein
  DESCRIPTION: B cell activation antigen; natural ligand
  DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
  NAME/KEY: signal sequence
  LOCATION: -34 to -1
  IDENTIFICATION METHOD: amino terminal sequencing of

IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.

RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-153-262-2

Query Match   100.0%; Score 1149; DB 3; Length 288;
Best Local Similarity 100.0%; Pred: No. 5.2e-113; Indels 0; Gaps 0;
Matches 216; Conservative 0; Mismatches 0;

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Qy    1  GLSHCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDNNIWPE   60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27  GLSHCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDNNIWPE   86

Qy   61  YKNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADPPTPS  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87  YKNRIIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADPPTPS  146

Qy  121  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||||||||||||||||||||||||||||||||
Db  207  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
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RESULT 6
US-08-479-744A-29
Sequence 29, Application US/0847974A
Patent No. 6084067

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
TOPOLOGY: linear
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain

LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262

US-08-479-744A-29

Query Match   100.0%; Score 1149; DB 3; Length 288;
Best Local Similarity 100.0%; Pred. No.5.2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy  61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy 121 ISDPEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 147 ISDPEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||||||||||||||||||||||||||||||||
Db 207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
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RESULT 7
US-08-280-757B-29
Sequence 29, Application US/08280757B
Patent No. 6130316
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
APPLICANT: Greenfield, Edward
TITLE OF INVENTION: No. 6130316e1 CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,757B
FILING DATE: 26-JUL-1994

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/101,624
  FILING DATE: 26-JULY-1993
  APPLICATION NUMBER: 08/109,393
  FILING DATE: 19-AUG-1993
  APPLICATION NUMBER: 08/147,773
  FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
  NAME: Mandragouras, Amy E.
  REGISTRATION NUMBER: 36,207
  REFERENCE/DOCKET NUMBER: RPI-004CP2
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (617) 227-7400
  TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 29:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 288 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
  MOLECULE TYPE: protein
  DESCRIPTION: B cell activation antigen; natural ligand
  DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
  FEATURE:
    NAME/KEY: signal sequence
    LOCATION: -34 to -1
    IDENTIFICATION METHOD: amino terminal sequencing of
    IDENTIFICATION METHOD: soluble protein
    OTHER INFORMATION: hydrophobic
  FEATURE:
    NAME/KEY: extracellular domain
    LOCATION: 1 to 208
    IDENTIFICATION METHOD: similarity with known
    IDENTIFICATION METHOD: sequence
  FEATURE:
    NAME/KEY: transmembrane domain
    LOCATION: 209 to 235
    IDENTIFICATION METHOD: similarity with known
    IDENTIFICATION METHOD: sequence
  FEATURE:
    NAME/KEY: intracellular domain
    LOCATION: 236 to 254
    IDENTIFICATION METHOD: similarity with known
    IDENTIFICATION METHOD: sequence
  FEATURE:
    NAME/KEY: N-linked glycosylation
    LOCATION: 19 to 21
    IDENTIFICATION METHOD: similarity with known
    IDENTIFICATION METHOD: sequence
  FEATURE:
    NAME/KEY: N-linked glycosylation
    LOCATION: 55 to 57
    IDENTIFICATION METHOD: similarity with known
    IDENTIFICATION METHOD: sequence
  FEATURE:
    NAME/KEY: N-linked glycosylation
    LOCATION: 64 to 66
    IDENTIFICATION METHOD: similarity with known
    IDENTIFICATION METHOD: sequence
  FEATURE:
    NAME/KEY: N-linked glycosylation
    LOCATION: 152 to 154
    IDENTIFICATION METHOD: similarity with known
    IDENTIFICATION METHOD: sequence
  FEATURE:
    NAME/KEY: N-linked glycosylation
    LOCATION: 173 to 175
    IDENTIFICATION METHOD: similarity with known
    IDENTIFICATION METHOD: sequence
  FEATURE:
    NAME/KEY: N-linked glycosylation
    LOCATION: 177 to 179
    IDENTIFICATION METHOD: similarity with known

  FEATURE:
    IDENTIFICATION METHOD: sequence
    NAME/KEY: N-linked glycosylation
    LOCATION: 192 to 194
    IDENTIFICATION METHOD: similarity with known
    IDENTIFICATION METHOD: sequence
  FEATURE:
    NAME/KEY: N-linked glycosylation
    LOCATION: 198 to 200
    IDENTIFICATION METHOD: similarity with known
    IDENTIFICATION METHOD: sequence
  FEATURE:
    NAME/KEY: Ig V-set domain
    LOCATION: 1 to 104
    IDENTIFICATION METHOD: similarity with known
    IDENTIFICATION METHOD: sequence
  FEATURE:
    NAME/KEY: Ig C-set domain
    LOCATION: 105 to 202
    IDENTIFICATION METHOD: similarity with known
    IDENTIFICATION METHOD: sequence
  PUBLICATION INFORMATION:
    AUTHORS: FREEMAN, GORDON J.
    AUTHORS: FREEDMAN, ARNOLD S.
    AUTHORS: SEGIL, JEFFREY M.
    AUTHORS: LEE, GRACE
    AUTHORS: WHITMAN, JAMES F.
    AUTHORS: NADLER, LEE M.
    TITLE: B7, A New Member Of The Ig Superfamily With
    TITLE: Unique Expression On Activated And Neoplastic B Cells
    JOURNAL: The Journal of Immunology
    VOLUME: 143
    ISSUE: 8
    PAGES: 2714-2722
    DATE: 15-OCT-1989
    RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262

US-08-280-757B-29

Query Match   100.0%;   Score 1149;   DB 4;   Length 288;
Best Local Similarity 100.0%;   Pred. No. 5.2e-113;
Matches 216;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
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Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTFDITNNLSIVILALRPSDEGTYECVVLKIEKDAFKREHLAEVTLSVKADFPTPS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTFDITNNLSIVILALRPSDEGTYECVVLKIEKDAFKREHLAEVTLSVKADFPTPS 146

Qy 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||||||||||||||||||||||||||||||||
Db 207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

GENERAL INFORMATION:
  APPLICANT: Ostrand-Rosenberg, Suzanne
  APPLICANT: Baskar, Sivasubramanian
  APPLICANT: Glincher, Laurie H.
  APPLICANT: Freeman, Gordon J.
  APPLICANT: Nadler, Lee M.
  TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
  NUMBER OF SEQUENCES: 4
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/159,135
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/147,772
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989

US-09-159-135-2
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262

Query Match   100.0%;   Score 1149; DB 4;   Length 288;
Best Local Similarity 100.0%;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy   121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy   181 NMTTNHSFMCLIKYGHLRVNQTFNWNTIKQEHFPDN 216
             ||||||||||||||||||||||||||||||||||||
Db   207 NMTTNHSFMCLIKYGHLRVNQTFNWNTIKQEHFPDN 242

RESULT 9
US-08-205-697A-19
; Sequence 19, Application US/08205697A
; Patent No. 6218510
; GENERAL INFORMATION:

RESULT 10
US-08-702-525-19
Sequence 19, Application US/08702525
Patent No. 6294660

GENERAL INFORMATION:
 APPLICANT: Sharpe, Sharpe
 APPLICANT: Borriello, Francescopaolo
 APPLICANT: Freeman, Gordon
 APPLICANT: Nadler, Lee
 TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory
 TITLE OF INVENTION: Molecules and Uses Therefor
 NUMBER OF SEQUENCES: 65
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 28 State Street

CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, Suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875
COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/205,697A
 FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: BWI-120
TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 288 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
US-08-205-697A-19 MOLECULE TYPE: protein

Query Match 100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy 61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
   ||||||||||||||||||||||||||||||||||||
Db 207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 11
US-09-450-798-2
Sequence 2, Application US/09450798
Patent No. 6319709

GENERAL INFORMATION:
 APPLICANT: Ostrand-Rosenberg, Suzanne
 APPLICANT: Baskar, Sivasubramanian
 APPLICANT: Glimcher, Laurie H.
 APPLICANT: Freeman, Gordon J.
 APPLICANT: Nadler, Lee M.
 TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, Suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/702,525
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/205,697
 FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: BWI-120CPUS
TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 288 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
US-08-702-525-19

Query Match 100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy 61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
   ||||||||||||||||||||||||||||||||||||
Db 207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875
COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/205,697A
 FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: BWI-120
TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 288 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
US-08-205-697A-19 MOLECULE TYPE: protein

APPLICANT: Sharpe, Arlene H.
APPLICANT: Borriello, Francescopaulo
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:

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OPERATING SYSTEM:  PC-DOS/MS-DOS
SOFTWARE:  Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER:  US/09/450,798
FILING DATE:  29-NOV-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER:  US/08/147,772
FILING DATE:  03-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME:  Mandragouras, Amy E.
REGISTRATION NUMBER:  36,207
REFERENCE/DOCKET NUMBER:  RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE:  (617) 227-7400
TELEFAX:  (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH:  288 amino acids
TYPE:  amino acid
TOPOLOGY:  linear
MOLECULE TYPE:  protein
DESCRIPTION:  B cell activation antigen; natural ligand
   for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY:  signal sequence
LOCATION:  -34 to -1
IDENTIFICATION METHOD:  amino terminal sequencing of
OTHER INFORMATION:  hydrophobic
IDENTIFICATION METHOD:  soluble protein
FEATURE:
NAME/KEY:  extracellular domain
LOCATION:  1 to 208
IDENTIFICATION METHOD:  similarity with known
IDENTIFICATION METHOD:  sequence
FEATURE:
NAME/KEY:  transmembrane domain
LOCATION:  209 to 235
IDENTIFICATION METHOD:  similarity with known
IDENTIFICATION METHOD:  sequence
FEATURE:
NAME/KEY:  intracellular domain
LOCATION:  236 to 254
IDENTIFICATION METHOD:  similarity with known
IDENTIFICATION METHOD:  sequence
FEATURE:
NAME/KEY:  N-linked glycosylation
LOCATION:  19 to 21
IDENTIFICATION METHOD:  similarity with known
IDENTIFICATION METHOD:  sequence
FEATURE:
NAME/KEY:  N-linked glycosylation
LOCATION:  55 to 57
IDENTIFICATION METHOD:  similarity with known
IDENTIFICATION METHOD:  sequence
FEATURE:
NAME/KEY:  N-linked glycosylation
LOCATION:  64 to 66
IDENTIFICATION METHOD:  similarity with known
IDENTIFICATION METHOD:  sequence
FEATURE:
NAME/KEY:  N-linked glycosylation
LOCATION:  152 to 154
IDENTIFICATION METHOD:  similarity with known
IDENTIFICATION METHOD:  sequence
FEATURE:
NAME/KEY:  N-linked glycosylation
LOCATION:  173 to 175
IDENTIFICATION METHOD:  similarity with known
IDENTIFICATION METHOD:  sequence
FEATURE:
NAME/KEY:  N-linked glycosylation
LOCATION:  177 to 179
IDENTIFICATION METHOD:  similarity with known
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IDENTIFICATION METHOD:  sequence
FEATURE:
NAME/KEY:  N-linked glycosylation
LOCATION:  192 to 194
IDENTIFICATION METHOD:  similarity with known
IDENTIFICATION METHOD:  sequence
FEATURE:
NAME/KEY:  N-linked glycosylation
LOCATION:  198 to 200
IDENTIFICATION METHOD:  similarity with known
IDENTIFICATION METHOD:  sequence
FEATURE:
NAME/KEY:  Ig V-set domain
LOCATION:  1 to 104
IDENTIFICATION METHOD:  similarity with known
IDENTIFICATION METHOD:  sequence
FEATURE:
NAME/KEY:  Ig C-set domain
LOCATION:  105 to 202
IDENTIFICATION METHOD:  similarity with known
IDENTIFICATION METHOD:  sequence
PUBLICATION INFORMATION:
AUTHORS:  FREEMAN, GORDON J.
AUTHORS:  FREEMAN, ARNOLD S.
AUTHORS:  SEGIL, JEFFREY M.
AUTHORS:  LEE, GRACE
AUTHORS:  WHITMAN, JAMES F.
AUTHORS:  NADLER, LEE M.
TITLE:  B7, A New Member Of The Ig Superfamily with
TITLE:  Unique Expression On Activated And Neoplastic B Cells
JOURNAL:  The Journal of Immunology
VOLUME:  143
ISSUE:  8
PAGES:  2714-2722
DATE:  15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO:  2: From -26 to 262
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Query Match       100.0%;   Score 1149;   DB 4;   Length 288;
Best Local Similarity  100.0%;   Pred. No. 5.2e-113;
Matches  216;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy      1  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLIMMSGDMNIWPE  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     27  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLIMMSGDMNIWPE  86

Qy     61  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLXYEKDAFKREHLAEVTLSVKADPPTPS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     87  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLXYEKDAFKREHLAEVTLSVKADPPTPS 146

Qy    121  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSODPETELYAVSSKLDF 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    147  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSODPETELYAVSSKLDF 206

Qy    181  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
           ||||||||||||||||||||||||||||||||||||
Db    207  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
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RESULT 12
US-08-403-253A-2
Sequence 2, Application US/0840325 3A
Patent No. 6352694
GENERAL INFORMATION:
APPLICANT:  June, Carl H., Thompson, Craig B., Nabel, Gary J.
APPLICANT:  Gray, Gary S., Rennert, Paul D.
TITLE OF INVENTION:  Methods For Selectively Stimulating Proliferation Of T-Cell
NUMBER OF SEQUENCES:  14
CORRESPONDENCE ADDRESS:
ADDRESSEE:  LAHIVE & COCKFIELD
STREET:  28 State Street
CITY:  Boston
STATE:  Massachusetts
```

COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,253A
FILING DATE: March 10, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
OTHER INFORMATION: soluble protein hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known sequence

PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262

US-08-403-253A-2

Query Match   100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.2e-113;
Matches 216; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy 61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPPS 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPPS 146

RESULT 13
PCT-US95-02576-19
Sequence 19, Application PCT/US9502576
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02576
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120CPPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match   100.0%;   Score 1149;   DB 5;   Length 288;
Best Local Similarity 100.0%;   Pred. No. 5.2e-113;
Matches 216;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||||||||||||||||||||||||||||||||
Db 207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 14

US-09-171-945-131
Sequence 131, Application US/09171945
Patent No. 6277599
GENERAL INFORMATION:
APPLICANT: Emery, Stephen
APPLICANT: Copley, Clive Graham
APPLICANT: Edge, Michael Derek
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
FILE REFERENCE: Monoclonal Antibody to CEA
CURRENT APPLICATION NUMBER: US/09/171,945
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR FILING DATE: 1996-05-04
PRIOR APPLICATION NUMBER: PCT/GB97/01165
PRIOR FILING DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 131
LENGTH: 473
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Sequence
US-09-171-945-131
OTHER INFORMATION: Description of Artificial Sequence: humanized

Query Match   100.0%;   Score 1149;   DB 4;   Length 473;
Best Local Similarity 100.0%;   Pred. No. 1.1e-112;
Matches 216;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||||||||||||||||||||||||||||||||
Db 207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 15
US-09-460-384-36
Sequence 36, Application US/09460384
Patent No. 6337316
GENERAL INFORMATION:
APPLICANT: EL TAYAR, Nabil
APPLICANT: BLECHNER, Steven
APPLICANT: JAMESON, Brad
APPLICANT: TEPPER, Mark
TITLE OF INVENTION: CD28/CTLA-4 INHIBITING PEPTIDOMIMETICS,
PHARMACEUTICAL COMPOSITIONS THEREOF, AND METHOD OF USING
SAME
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/460,384
;     FILING DATE: 13-Dec-1999
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: PCT/US98/12312
;     FILING DATE: 11-JUN-1998
;     APPLICATION NUMBER: US 60/049,470
;     FILING DATE: 12-JUN-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: YUN, Allen C
;     REGISTRATION NUMBER: 37,971
;     REFERENCE/DOCKET NUMBER: EL TAYAR-1A
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (202) 628-5197
;     TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 36:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 208 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-460-384-36

Query Match             95.9%;  Score 1102;  DB 4;  Length 208;
Best Local Similarity   100.0%;  Pred. No. 2.8e-108;
Matches  208;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    9 VIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRTIFD 68
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 VIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRTIFD 60

Qy   69 ITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPT 128
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPT 120

Qy  129 SNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSF 188
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 SNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSF 180

Qy  189 MCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||||||||||||||||||||||||
Db  181 MCLIKYGHLRVNQTFNWNTTKQEHFPDN 208

Search completed: October 17, 2002, 16:36:35
Job time : 15 secs
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